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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model	March 21, 2004, 02:21:01 ; Search time 12121 Seconds (without alignments) 11646.585 Million cell updates/sec	US-09-817-198C-1 3257 1 tgcccgctgcccgccgcagaaaaaaaaaaaaaaa	IDENTITY NUC Gapop 10.0 , Gapext 1.0
cleic se	March 2	US-09-8 3257 1 tgccc	IDENTIT Gapop 1
OM nucleic - nuc	Run on:	Title: Perfect score: Sequence:	Scoring table: IDENTITY_NUC Gapop 10.0 ,

Total number of hits satisfying chosen parameters:

3470272 segs, 21671516995 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

GenEmbl:* Database :

gb ba: *
gb htg: *
gb ov: *
gb ov: *
gb pat: *
gb pt: *
gb v: * em_om:* em_or:* em_ov:*

em_htgo_hum:* em_htgo_mus:* em_htgo_other:* em_htg_hum:*
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em_htg_mus:* em_htg_pln:* em_htg_rod:* em_htg_mam:* em_htg_vrt:* em_sy:* em_pat: *
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em_sts: *
em_un: *
em_vi: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	t Score	Query Match	Length	DB	ID	Description
	303	r		σ	BC040679	6190
	2696	82	190517	σ	CNS01DX4	3022 Humar
	1423	43	2210	σ	690	25
	1192	36	7924	9	704	7040 Segue
	1192	36	7924	9	AX348456	26
υ	1160	35	7924	9	AX347041	41
	1160	35	7924	9	AX348457	57
	1000	30	1054	9	AX399903	2
	998	26	895	9	AX014147	
-	866	26.6	895	9	BD205055	Š
-	œ	25	3139	2	BC027769	S.
~	9	13	929	9		AX781147 Sequence
Н	577	17	945	2	RATRAB15X	M83679 Sprague-Daw
-	477.	4	481	ø	AX396088	AX396088 Sequence
υ 1		ന	463	9	AX334820	AX334820 Sequence
-	423	13	270654	7	AC096084	AC096084 Rattus no
-	416	12	2560	10	BC013790	BC013790 Mus musc
-		11	410	9	AX779778	AX779778 Seguence
-	378	11	190726	~	AC132331	AC132331 Mus muscu
~	338	10		S	BC063736	
~		6	313	9	AX341683	Seguenc
N	234	7		9	BC002977	BC002977 Homo sapi
	234	7		ō	AK025165	AK025165 Homo sapi
10	230	7		6		S53268 Homo sapien
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BC040679 3326 bp mRNA linear PRI 11-DEC-2003 Homo sapiens RAB15, member RAS onocogene family, mRNA (cDNA clone MGC:42319 IMAGE:4817835), complete cds. BC040679.2 GI:34783346 Homo sapiens (human) RESULT 1 BC040679 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

ALIGNMENTS

Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 3326)
Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

REFERENCE AUTHORS

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220

240 340

280

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781 TGTGGGGCACCCCACACGACACCCCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGGAG
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               26. .343
/note="RAB; Region: Rab subfamily of small GTPases"
/db_xref="CDD:cd00154"
                                                                                                                                              DB 9;
                                                                                                                                         Score 3030.2;
Pred. No. 0;
0; Mismatches
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatcherko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Mokernan, K.J., Mulley, S.J., Bosak, S.A., McKearn, P.M., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Luix, Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butferfield, Y.S., Kzzywinski, M.I., Skalski, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Schein, J.E., Jones, S.J. and Marra, M.A. Schein, J.E., Jones, S.J. and Marra, M.A.
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Location/Qualifiers
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SKKYTIEVDGGTKVRLQIMOTAGQERVQTTKQYSYRRAQGIFLYVDISSERSYQHIMKW
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SLLGIRLMRSRNGRWEESKGSSWRRSWAWTSMKQVPAPISTLKSHSRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susama Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Danne Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submitseion
Submitted (29-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced gi:26251822.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and Plero Carninci (RIKEN)
Toshiyuki and Plero Carninci (RIKEN)
EMA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/protein id="AAH44679.2"
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/db_xref="taxon:9606"
/clone="MGC:42319 IMAGB:4817835"
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Proc. Natl. Acad. Sci. U.S.A. 9
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'gene="RAB15"
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JOURNAL
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REFERENCE
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COMMENT
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361 AGAGGGTGCCTCACCGGGGAAGGCAAGGCGAGGGCCAGATGGGAAGGCAAATGCTTCCAG 420
                                                                                                                                                    41 AGTCATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGT
                                                                                                                                                                                                                                                                                                             GGGCAAGACCTGCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTC
                                                                                                                                                                                                                                                                                                                                                         61 GGGCAAGACCTGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CACCATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGCATCAAGTGCGGAT
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                                                                                                                                                                                                                             AGTCATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGAT
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                                                                            Gaps
Length 3326;
                                                                        8; Indels 132;
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540 509 9 569 99 720 689 780 749 840 809

CDS

FEATURES

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3120 TCGTCACCACCTCTGCTGCTGTTGAGACTCCATCCAGGCACGCCCCCG 3179 3190 CTCCTGAGCCTCCACTATCTGTGAGCTCCAGGCACGCCCCCG 3179	RESULT 2 CNS01DX4 CNS01DX4 LDCUS DNA linear PRI 17-MAY-2001 LDCUS DEFINITION Human chromosome 14 Of Homo sapiens (Human), complete sequence. ACCESSION AL139022.4 GI:14148954 KEYWORDS SOURCE Homo sapiens (human) CRGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human)	REFERENCE I (bases 1 to 190517) AUTHORS Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., AUTHORS Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, B., Artiguenave, F., Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J. TITLE Sequencing of the human chromosome 14 JOURNAL Unpublished REFERENCE (bases 1 to 190517) AUTHORS Genoscope.	Submitted (17-MAY-2001) Genoscope - Centre National de Sequenc BP 191 91006 ENRY cedex - FRANCE (B-mail : seqref@genoscope.cm - Web : www.genoscope.cns.fr) On May 18, 2001 this sequence version replaced gi:10798506	The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : C-2509G16 (AC=AL355076) Downstream BAC (overlapping the SP6 end) : C-2300N4	0 1 2 3 445 45 460 49 11521 500 60 - 69 11521	79 : 89 : 99 : entage of Local 1.

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                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/codon_start=1
/product=hrypochetical protein"
/product=hrypochetical protein"
/protein id="CRE45901.1"
/db_xref="G1:34165091"
/db_xref="G1:34165
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/gene="DKF20686J06205"
/gene="DKF2068J06205"
/nore="shirlarity to GTP-binding protein rabl5 (Rattus norvegicus)"</pre>
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Pred. No. 0;
0; Mismatches 12; Indels 0;
/mol_type="mRNA"
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/map="14q23.3"
/clone="DKFZp686J06205"
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Best Local Similarity 99.2'
Matches 1431; Conservative
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Neuherberg, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz.heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2210)

Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

The German Human cDNA Consortium
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                  160259 TGTGACGGGTGAACTTCGTGTACTGTGTCTCGGGTCCATATATGAATTGTGAGCAGGGTT
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BX640825
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/mol_type="unassigned DNA" /db_xref="texon:32630" /note="chemically treated genomic DNA (Homo sapiens)" Query Match 36.6%; Score 1192.8; DB 6; Length 7924; Best Local Similarity 75.8%; Pred. No. 1.6e-287; Matches 1476; Conservative 0; Mismatches 472; Indels 0; Gaps 0	Qy 1276 GATGCTTCTTCCTCTTCCCCACCCCACCCCACTGTGCCATGTGCCTTGCCTTCCCC 1335	0 1396 GCCTGGGGCCTACCTCTACCCGACCGGCGCCTGCTTGCCTTGCTTG	241 GAGGGTGGTAGGGATAAAAGTTATTTTTTTTTTTTTTT	361 GGGTAAGAGAGTTTTGGGGTTAGTGATTTGTTAGTTTAATTTTTT	1756 CCAGGGAAGCATTIGCACGCAGGGGGAATGTAGCAACAGCAGGGCCTCCTAGGCCC 181 481 TTAGGGATAGTTIGTATGATAGGAGGGAATGTAATAGTAAGGTTTTTTTT	QY 1876 CTRGCCARGCRACCARGGTTCTCCTGGGACCCCAAAGTTTATGGAGAAAGAGGACAAGAC 1935 Db 601 TTAGTTTTTAGTAATTAAGGTTTTTTTGGGATTTAAAGTTTATGGAAAGGGTAAAGAT 660 QY 1936 TTCATGGGAAGAGAAGAAAGGAAGGAAGGGTAGAAAAGCTTTGGTGCTTTTTTTGGCC 1995 Db 661 TTTATGGGAAGAAGAAGAAGATTTTGGGTAGAAAACGTTTGGTGTTTTTTTT	1996 TITAAGACAAAGGGCTCATCTTGCCTCTACCTCCTGATAGGCTTGAGGGTTTGCCAACC	Oy 2116 GTTTCTTTAACCCCAAGACTAGCTCGTAGGAGGCCTTTAAAGACGGAACA 2175
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Method and nucleic acids for pharmacogenomic methylation analysis
Patent: WO 0202806-A 151 10-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers 61 AGTGATTTGCGAAGTGTGGAGTATCGAGGTAGGAGGAAACGGTAATTAGGGAGTTTTCGA 601 TTAGTTTTTAGTAATTAAGGTTTTTTTGGGATTTTAAAGTTTTATGGGAGAAAGGTAAAAGAT 181 TCGTTTGTTTTTTGGGGAATTGAGTTTAGAGGTAGGTGTTTTAGAGAAGGAAATAAAAT 1576 ATTICICICCACCIGGCICCCAAAITIAAAGAIGIGGACCAAGGCCIGIGGGIACICCAG 301 ATTITITITITIATTIGGTTTTAAATTTTAAAGATGTGGGATTAAGGTTTGTGGGTATTTAG GGGCAAGGAGCCCTGGGGTCAGTGACACTGTCAGGCCAACCATGCACTCCACAAAGGG 361 GGGTAAGGAGAGTTTTGGGGTTAGTGATATTGTTAGGTTAATTATGTTATTTATAAAGGG 421 GAGTATTTGGAAATGAAGGATTAGTTTTTATGTATTAGGTTAAGAGTAAGTAAGGTTGG CATCTTCCATTTCTTAGGTAAGAGCATTTCCTCAGACTCCCAGGCGGAGGACTGAGC CTAGCCTTCAGCAACCAAGGTTCTCCTGGGACCCCAAAGTTTATGGGAGAAGGGCAAAGAC TTCATGGGAAGAGAAGGAAGGCCCTGGGTAGAAACGCTTGGTGCTGTTCTCTTTGGCC 1. .7924 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="texon:32630" /note="chemically treated genomic DNA (Homo sapiens)" CCGCCTGCCTCTTTGGGGAACTGAGCTCAGAGGCAGGTGCTTCAGAGAAGGAAACAAAAT 1516 GAGGGGTGGCAGGGATAAAAGTCACCTCCATTCTCTACCTCCCATGCAGCATGAACACA AGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAACAGCAACCGGGGGAGTCCTCGA Gaps Length 7924; ö Indels Query Match
36.6%; Score 1192.8; DB 6;
Best Local Similarity 75.8%; Pred. No. 1.6e-287;
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-2002; recercargrecearegeerrecerag TTGAGGCCCAGACTGTTAAGCAGGCTCTGC ted genomic DNA (Homo sapiens)" Gaps 0.8; DB 6; Length 7924; 1.7e-279; ches 512; Indels 0; onstruct" DNA" DNA

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Patent: WO 0218424-A 74 07-MAR-2002;
HYSEQ, INC. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PAT 07-SEP-2000
                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                  Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and Pilarsky, C.
Human nucleic acid sequences of bladder tumour tissue
Patent: WO 995447-A 12 28-0cT-1999,
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
           Sequence 12 from Patent W09954447. AX014147
                                                              AX014147.1 GI:10040594
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Best Local Similarity 99.5%;
Matches 879; Conservative
                                                                                         Homo sapiens (human)
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                                                                           GCCCGCTGCCCGCCCGCTCCCGGCCCCGCTGGCCCAGTCATGGCGAAGCAGTACGA
                                                                                                           CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA
                                                                                                                                                                                                                                  GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG
                                                                                                                                                                                                                                                                                            242 GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTT
                                                                                                                                                                                                                                                                                                                 278 GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTT
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                Indels
Pred. No. 2.3e-239;
0; Mismatches 4;
99.68;
              Matches 1002; Conservative
Best Local Similarity
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134 ATAGCTTAGATGGTGGAAAGCAAAGGAGGAGCAGGAAGTTGTAAATCACTGGCTAATGAGA 193		QY 2958 CCCTABACTITIGGIGGCTGGGGCATGTCTTGAGGCCCAGACTGTTAAGCAGGTTGC 3017 bb 613 CCCTAAACTITIGGIGGCCTGGGGCTGTCTTGAGGCTGTTAAGCAGGTTGG 672 QY 3018 TGGCCTGTTACTCGTCACCACCTGTGTGTTGAGACTCCATCCA	RESULT 11 BC027769 BC027769 BC027769 BC027769 BC027769 BC027769 BC027769 BC027769 BC027769 ACCESSION BC027769 BC027769.1 GI:20380721 KEYMORDS MGC. SOURCE Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus (house canadata; Vertebrata; Buteleostomi;	REFERENCE (Caramedia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Caramedia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus. Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buercow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Oy 3018 TGGCCTGTTTACTCGTCACCACCTGGCTGTCTTAGACTCCATCCA	RESULT 10 BD205055 BD205055 LOCUS BD205055 LOCUS BD205055 LOCUS BD205055: 1 G1:33014825 VERSION BD205055: 1 G1:33014825 KEYWORDS Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) REPERENCE REPRENCE: Natazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 895) AITHURS AITHURS AITHURS AITHURS ACHIEF SCHOOL AND	Rosenthal, A. Human nucleic acid sequence originating in cystic cancer Parent: JP 200251203-A 9 23-APR-2002; METAGEN GESELLSCHAFF FURR GENOM FORSCHUNG MBH OS Homo sapiens (human) BN JP 200251203-A/9 PN JP 200251203-A/9 PP 15-APR-1999 JP 2000544779 PP 21-APR-1999 DE 198 18 619.3 PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PI EDGAR DAHL, PI ANDRE ROSENTHAL PI ANDRE GOTAL 4/7, CO7XL6/18, C12NS/10, C12P21/02, C12P21/08, C12C12N15/00, PC C12N15/00, PC GTXL4/47, C07XL6/18, G12NS/10, C12P21/02, C12P21/08, C12C12N15/00, PC Human nucleic acid sequence originating in cystic catternal process.	FH Key Location/Qualifiers FT Source 1895 FT Source 1895 Source 1895 Accordanism="Homo sapiens (human)'. FEATURES Location/Qualifiers Accordanism="Homo sapiens" Amol_type="genomic DNA" Abo_xref="taxon:9606" Abo	2358 AGAACCTACTTCCTTACTCCTCAAAAGTGGGGAAAGAACTCCTCTCTCT

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484 381 544 441 604 501 664 561 724 621 784 681

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GCCTCCTGTGA-CCCCAGAATGTGCTGC-----GACCACCCCAGGCTCCTGGG 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCACAAAGCAGTACTATCGGCGCGCGCAGGGGATATTTTTGGTCTATGACATTAGCAGCG 321
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                                                                                                                                                                                                                                                                                                TGATCGGGGACTCCGGGGTGGGCAAGACCTGCCTGCTGTGCCGCTTCACCGACAACGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742 CAGGGGAGCCGGGGCTTTGCCCTGCTGCTGTCCTCTGTGATGACCCTATTGAGTATC
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                                                                                                                                   Gaps
                                                                                                                                 Indels 165;
                                                                            Length 3139;
                                                                            Score 813; DB 10;
Pred. No. 2.4e-192;
0; Mismatches 640;
     db xref="CDD:cd00154"
                                                                            Query Match 25.0%;
Best Local Similarity 67.4%;
Matches 1662; Conservative
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Tissue Procurement: Jeffrey Green M.D.
The Institutes of Health Intramural
Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC)
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bootstrand, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Boutter, S., (Guan, X., Gupca, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, O. L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thouchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 55 Row: d Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19527265.
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/translation="WAKQYDVLRELLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVD
FKWKTIDVDGIKVRIQIWDTAGOGRVQTITKQYYRRAQGIFLVVDISSERSYQHIMKW
VSDVDEYAPEGVVQKILIGNKADEDGKRQVGREQGQQLAKEYGNDFYBTSACTFLINIKE
SFTRLTELVLQAHRKELDGLRTRASNELALAELEEDEGKFEGPANSSKTCWC"
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Juctal Carcinoma. 5 month old virgin mouse."
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Worllay, D.K., Muran, D.D., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Banchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schalus, D.E.,
Schnerch, A., Scháin, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229. .720
/note="RAB; Region: Rab subfamily of small GTPases"
                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/product="Rabl5, member RAS oncogene family"
/protein_id="AAH27769.1"
/db_xref="G1:20380722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/db_xref="MGI:1916865"
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/organism="Mus musculus"
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/clone_lib="NCI_CGAE
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/strain="FVB/N"
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                                                                                   2143 AAGTTTCTTTAACCC--TGTGGTTCAAGAGTAGCTTGAAGGAGGCCCCTGAAAAAAAC 2200
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0; Mismatches 43;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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ACGACGGTCAAGGCTGGAGTCAAGGCCACTTCAAG-----ATTCCTTAGTGCATCTCGT 1177
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/translation="MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVD
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VSDVDEYAPEGVQKTLIGNKADEBOKKQVGREQGQQLAKEYGMDFYETSACTVLNIKE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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GECCCAGACTGTTAANCAGGNTCTGCTGGCCTGTTTACTCGTCACCACCTGCCTGC
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Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds.
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rabls, a novel low molecular weight GTP-binding percifically expressed in rat brain
J. Biol. Chem. 267 (9), 5768-5775 (1992)
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/mol_type="mRNA"
/strain="Sprague-Dawley"
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'tissue_lib="LAMBDA_ZAPII"
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tissue_type="brain"
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LMW GTP-binding protein.
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Rattus norvegicus
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Compositions and methods for the therapy and diagnosis of colon
                                                                                                                                                                                                                                                 1 GTTGCTTCCTTGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACACATCACACTGGGG
                                                                                                                                                                                                                                                                                                           121 TATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTCAGCTTTCCCTGAAGATCAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GGTGCCATTCATTGTCTTTCTCTCTAGCCCCTCAGGAAGAAGAAGAACTATATTTGTACT
                                                                                                                                                                                                                            2582 GTTGCTTCCTTGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGG
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                                                                                                                                                                  Length 481;
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14.7%; Score 477.4; DB 6;
Best Local Similarity 99.4%; Pred. No. 2.6e-108;
Matches 478; Conservative 0; Mismatches 3;
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Patent: WO 0194629-A 5329 13-DEC-2001;
Avalon Pharmaceuticals (US)
              cancer.
Patent: WO 0212328-A 303 14-FEB-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 bp D1 Sequence 5329 from Patent WO0194629. AX334820 AX334820.1 GI:18125539

    .481
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    .463
/organism="Homo sapiens"

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                                                                                                                                              Gaps
                                                                                                                                              1,
                                                                                                  Length 463;
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                                                                                             Score 438.8; DB 6;
Pred. No. 1.2e-98;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3210 TATTTCAAACCACCACAAAAAAAAAAAAAAAAA 3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="unassigned DNA"
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Best Local Similarity 99.3%;
Matches 451; Conservative
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Search completed: March 21, 2004, 08:59:33 Job time : 12136 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                 Copyright
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- nucleic search, using sw model OM nucleic

March 21, 2004, 02:17:36; Search time 1147 Seconds (without alignments) 12063.105 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

3373863 segs, 2124099041 residues

Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 29Jan04:* 1: geneseqn1980s:* 2: geneseqn1990s:* •• Database

geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2000s:* geneseqn2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:

SUMMARIES

			•				
Res	Result No.	Score	% Query Match	* Query Match Length	DB	ID	Description
	1	3257	100.0	3257	7	AAD47168	Aad47168 Human Ras
υ	N	2696.6	82.8	3240	4	AAK82285	
	m	2696.6	82.8	28770	7	AAD47169	
	4	1568.2	48.1	1666	c	AAC75813	Aac75813 Human ORF
	Ŋ	1192.8	36.6	7924	9	ABK40069	Abk40069 Human che
	9	1192.8	36.6	7924	9	ABL34138	Abl34138 Human imm
υ	7	1160.8	35.6	7924	9	ABK40070	_
υ	σ,	1160.8	35.6	7924	9	ABL34139	Abl34139 Human imm
	σ	1160.6	35.6	2021	4	AAS27053	Aas27053 cDNA enco
	10	1160.6	35.6	2021	σ	ADB93231	Adb93231 Human cDN
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υ	16	438.8		463	9	ABL66992	Abl66992 Thyroid c
	17	424.4		458	œ	ACH33636	Ach33636 Human end
	18	313.4	9.6	320	~	AAT25457	Aat25457 Human gen
	4	307	9.4	313	9	ABL38341	
	20	.229	7.0	1986	4	ABA09160	Aba09160 Human rab
	21	228.4	7.0	2411	9	ABQ54410	Abq54410 Human ova
	22	217.8	6.7	1161	4	AAH75182	a
	23	217.8	6.7	1265	9	ABV78060	Abv78060 Hypoxia-r

Aas60878 Human can	Aas60884 Human can	Aas60893 Human can	Aas60895 Human can	Abv25781 Human pro	Abv30037 Human pro	Aah13912 Human cDN	Aah04301 Human cDN	Adb12721 Human pol	Adb52880 Primary r	Aac01700 Human sec	Aaa40104 Human Rab		Aaa96887 Nucleotid	Aaf16196 Human pro	Aah17889 Human cDN	Aas71453 DNA encod	Abl29661 Drosophil	Abx04179 Human mRN	Aaa40109 Canine Ra	Aaf18072 Lung canc	Aas87552 DNA encod
4 AAS60878	1 AAS60884	1 AAS60893	1 AAS60895	5 ABV25781	5 ABV30037	1 AAH13912	1 AAH04301	3 ADB12721	9 ADB52880	3 AAC01700	3 AAA40104	3 AAA40108	3 AAA96887	3 AAF16196	1 AAH17889	5 AAS71453	1 ABL29661	5 ABX04179	3 AAA40109	3 AAF18072	5 AAS87552
2497 4	2497 4	2497 4	2497 4	2497 5	2497 5	3077 4	866 4	1859 8	991	412 3	716 3	861 3	956	1537 3	3533 4	674 5	2247 4	3164 6	888	1274 3	893 5
6.7	6.7	6.7	6.7	6.7	6.7	6.7	9.9	6.4	6.2	6.2	6.1	6.1	6.1	6.1	6.1	6.0	6.0	6.0	6.0	5.9	5.8
217.8	217.8	217.8	217.8	217.8	217.8	217.8	214.2	209	203.2	202.6	2007	2007	198.4	198.4	198.4	196.8	196.6	195.6	195.2	192	188.6
24	25	56	27	28	29	30	31	c 32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAD47168 standard; cDNA; 3257 BP. (first entry) 24-FEB-2003 AAD47168; AAD47168

RESULT 1

Human Ras-like protein encoding cDNA.

Human; Ras-like protein; inflammation; cell proliferation; apoptosis; immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis; parkinson's disease; aschexia; myocardial infarction; osteoporosis; atherosclerosis; glomerulonephritis; crohn's disease; irritable bowel syndrome; multiple sclerosis; osteoparthritis; allergy; pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic; Sjogren's syndrome; infection; transgenic; gene therapy; noctropic; gout; neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic; ophthalmological; tranquilliser; cancer; stroke; Grave's disease; AIDS; asthma; anaemia; drug screening; gene; ss.

Homo sapiens

"Human Ras-like protein" Location/Qualifiers 45. 683 /*tag= b /product= ". 684. 3257 /*tag= c ø ...44 *tag= Key 5'UTR 3'UTR CDS NAME OF A STANCE O

WO200277193-A2.

03-OCT-2002.

27-MAR-2002; 2002WO-US009328.

27-MAR-2001; 2001US-00817198.

(PEKE) PE CORP.

Ye J, Di Francesco V, Beasley EM; San W,

WPI; 2003-018913/01. P-PSDB; AAE29096.

New isolated human Ras-like protein polypeptide, useful for diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma or stroke.

Claim 4; Page 73-74; 82pp; English

nucleic acid. The Ras-like protein and DNA is useful in the development of human therapeutics and diagnostic compositions. They are useful in the diagnosis, protein and respectable.

In the diagnosis prevention and treatment of inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS and other infectious or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia, ischaemic injuries e.g. myocardial infarction, stroke or reperfusion injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or careforming as disease, disease, glomerily allergies, atcopic dermatitis, atherosclerosis asterma, anaemia, crohn's disease, disease, glomerily adjaced such artitable bowel syndrome, lupus erythematosus, multiple sclerosis, osteoarthritis, pancreatitis, aucoimmune thyroiditis, rheumatoid arthritis, Sjogren's syndrome, cueitis, trauma, or viral, bacterial, fungal, parasitic, protozal or helminthic infections. The antibodies of the invention are useful in pharmacogenomic analysis or for tissue typing. The transgenic animals are and evaluating modulators of its activity. Ras like protein, and identifying and evaluating assays and its bNA is used in gene therapy. The present sequence is human Ras-like protein ecoding cDNA corresponding relates to human Ras-like protein and its invention

Sequence 3257 BP; 793 A; 892 C; 870 G; 702 T; 0 U; 0 Other;

360 120 120 180 240 240 300 420 420 480 540 540 121 GCGGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTTGACTTTA 180 AGCAGAAACGGCAGGTGGGAAGAGAGAGAAGAGCAGCAGCTGGCGAAGGAGTATGGCATGG 480 9 9 ACTICIAIGAAACAAGIGCCTGCACCTCAACCTITAAAGAGTCATICACGCGTCTGA TGCCCGCTGCCCGCCGCAGTTCCCGGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACG reccecrecceccecaerrecceccecreccecaercarecearacearacearace ATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCTGT GCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTA AGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAG AGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAG GGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGGATATTTT TGGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACG TGGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGG AGCAGAAACGCCAGGTGGGAAGAGAGCAAGGGCAGCAGCTGGCGAAGGAGTATGGCATGG Actrictardaaacaacreccrecaccaccreacarraaacaccarracaceccrea Gaps ö Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Batches 3257; Conservative 0; Mismatches 0; Indels 0; 241 7 61 121 181 181 241 301 301 421 361 421 481 481 ò 셤 ઠે ò 셤 ઠે 셤 ò 쉽 g ò 셤 8 ઠ

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	Oy Qa	601	ATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGCAAACCCGAGGCCCAGCGAACT
	6	661	CTTCGAAAACCTGCTGGTGCTGAGTCCTGTGGGGCACCCCACACGACACCCTCTTCC 720
	ò 8	721	CTCAGGAGGCCCGTGGGCA
	රු ය	781	GTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCTGCCTG
	S da	841	CTGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCC
	λδ Dp	901	GCCTGTTTCCCC
	δγ	961	ACCATCCCGCACCCACCAGCAACAGCCAGGGCTGGAGTCCAGGCCACTTTCAGC
	oy qa	1021	CTTTCTCCGTGCATCC
	oy Q	1081	TGACCCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAACCCCGTCCCCCGTGTGT 1140
	& g	1141	CCTGCTGTGTGCAGCTCGCTCTTTCCTTCCTAAGCTATCCAAGGGATGGACCCAG 120
	ò q	1201	GCTCGTGGGGAGGTTCCACCTTGGATCCAGGAAGACCCTCCACCCTGCCTCGTGGTG 12
	λ O	1261	
	- 6 6	1321	TGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGAAACAGCAA 13
	\$ 8	1381	TICCTCGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCGGAGCTTTG 14
	ζ q	1441	AGAGGCAGGTGCTTCAG 15 GAGGCAGGTGCTTCAG 15
	ò 8	1501	agaaggaaacaaaatgagggggggggataaaaagtcacctccattctctacctccca 1560
	ò	56	TGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCAAGGC 162.
,	g Yo	1561	TGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCAAGG CTGTGGGTACTCCAGGGGCAAGGAGACCCTGGGGTCAGTGACACTGTCAGGCCAACCA

Db 2701 ATATTGGGCATTCATTCTCTCTAGACCAGTATTTCAGCTTTCCCTGAAGATCAGCA 2760 Qy 2761 GGGTGCCATTCATTGTCTTTCTCTCTAGCCCCCTCAGGAAGAAGACGACTATATTTGTAC 2820 Db 2761 GGGTGCCATTCATTGTCTTTCTCTCTCAGGAAGAAGAAGAAGAACAATATTTGTAC 2820 Qy 2821 TGTACCCTAGGGGTACAGGAAAACAAACAACAATACAAT	RESULT 2 ANK82285/C ID AAK82285/C XX XX AC AAK82285, XX AC AAK82285, XX TOT-NOV-2001 (first entry) XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37097. XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; XX Homo sapiens. XX Homo sapiens. XX Homo sapiens. XX NO-200157182-A2. XX NO-300157182-A2. XX NO-300157183-A4. XX XX NO-300157183-A4. XX XX NO-300157183-A4. XX XX XX NO-300157183-A4. XX XX NO-300157183-A4. XX XX XX XX XX XX XX XX XX
	TGGGCGAGGCCTAGGAAGAGGGTCATTCTTAAGCCACATTAGCTGCATGCGTGGCTG TGGGCGAAGCGAA

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2000US-0231413P

2000US-0231414P

2000US-023200BP

2000US-023239P

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(HUMA-) HUMAN GENOME

Ruben SM Barash SC, Rosen CA,

NPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 37097; 3071pp + Sequence Listing; English

AMXS4951 to AAX64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the

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protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
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Location/Qualifiers	replace(206, -) /*tag= a /*tandard name= "Single nucleotide polymorphism"	/tag b /traduct= "Human Ras-like protein" /traduct= "Human Ras-like protein" /traduct	7.tdg= 2.554 7.tdg=	replace(*503,1) /taga replace(8175,A)	<pre>/*tag= i /*tadard name= "Single nucleotide polymorphism" replace(10515.C)</pre>	<pre>/*tag= g /standard_name= "Single nucleotide polymorphism" replace(13034,C)</pre>	/ rads n // ftandard_name= "Single nucleotide polymorphism" /replace13781,C) /*tad= i	ard name= "Single nucleotide 14050, C)	/standard name= "single nucleotide polymorphism" replace (14273, -) /אומר אימר אימר (14273, בים אימר אימר)	<pre>/*tag= k /standard name= "Single nucleotide polymorphism" /*tagle (17582,C) /*tagle</pre>	Single nucleotide	<pre>/standard_name= "Single nucleotide polymorphism" /*role (18074, TC) /*role</pre>	/standard name= "Single nucleotide polymorphism" replace(19328,T)	<pre>/*tag= o /standard_name= "Single nucleotide polymorphism" replace(19570,G)</pre>	<pre>/*tag= p /*tadard_name= "Single nucleotide polymorphism" replace(20892,T) /*tag= q</pre>	Ξ.	/*tag= r 21616. :22462 /*tag= s	2246322523 /*tag= t		/23/52305/ //tag= v		2371223801 /*tag= x 27802 -23802	•		/*Lay= aa 2561425769 /*tag= ab
Homo sapiens. Key	variation	exon	intron	variation variation	variation	variation	variation	variation	variation	variation	variation	variation	variation	variation	variation	exon	intron	exon	intron	exon	ıntron	exon	exon	intron	exon
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	Qy 2513 AGTIGTAAATCACTGGCTAATGAQAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGAC 2572	QY 2573 TAGGCTGGAGTTGCTTCCAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACATC 2632 	2633 ACACTGGGGCTAGGGAAGTAGGTGATGCCAGCCTCAAGTCTGTCT	DD 940 MCACIGGGGGCAGGGAAAGIGAIGCCIGAGCCICICAGGIGICIGIC	Db 880 GAGAAGTTATATTGGGCAGTGGCTCCCAATCTGTGGACCAGTATTTCAGCTTTCCCTGAAG 821	QY 2753 ATCAGGCAGGTGCCATTCATTGTCTTTCTCTCTAGCCCCCTCAGGAAAGAAGGACTAT 2812	QY 2813 ATTIGIACTGTACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACT 2872 Db 760 ATTIGIACTGCCTAGGGGTTCTGGAAGGGAAAACGAAAACATGGAATCAGATTCTATAGACT 701	2873 GATAGGCCCTATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGTATG	700 GATAGGCCCTATCCACAAGGGCCCATGACTGGGAAAAGGTATGGG	GGAITTTAGGGTGCAGCTACCCTAAACTTTTGGTGGCCTGGGGCATGTCTGAG 	QY 2993 GCCCAGACTGTTAAGCAGGCTCTGCTGGCTGTTTACTCGTCACCACCTCTGCACCTGCT 3052 Db 580 GCCCAGACTTAACCAGGCTCTGCTGGCTGTTTACTCGTCACCTCTGCTGCTTCTTCGTTGCTCACCTCTTGCTGCTTGCT	3053 GTCTTGAGACTCCAGGCCCCAGGCACGCCTGCTCCTCCCCAGGCTCCATATCCCC	GICTIGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCC	QY 3113 TGTGACGGGTGAACTTCGTGTACTGTGTCTCGGGTCCATATATGTAGATTGTGAGCAGGGTT 3172	Oy 3173 CATCTATTTAAACACAGATGTTTACAAAATAAAGATTATTTCAAACCACC 3223		KESULT 3 AAD47169 ID AAA47169 standard: DNA: 28770 BP.	AAD47169;	XX DT 24-FEB-2003 (first entry)	AA DE Human Ras-like protein encoding gene.	Human; Ras-like protein; inflammation; cell proliferation;				An Opinimalmological; clangulliser; cancer; scloke; orave's ulsease; Albs; .XX asthma; anaemia; drug screening; gene; chromosome 14; ds.

2562 TGCCAGGGGAGAGGAGGAGACACTGGACTAACCTGTGCCCTTTGGTTTCCAGTCATTCAC 25621

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++++	variation variation	e(26465,A) ac ard_name= e(26472,G)	Single	"Single nucleotide polymorphism"
+++	variation	ad ard_name= e(28071,T)	Single	"Single nùcleotide polymorphism"
	variation	ae ard_name= e(28096,G)	"Single	nucleotide polymorphism"
F F F 1	variation	af ard_name= e(28403,G)	"Single	nucleotide polymorphism"
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×Z	WO200277193-A2.		1	•
×Θ	03-OCT-2002.			
× &	27-MAR-2002; 200;	2002WO-US009328.		
× &	27-MAR-2001; 200	2001US-00817198.		
׫	(PEKE) PE CORP.			
X H	Gan W, Ye J, D	Di Francesco V, B	Beasley	EM;
X & &	WPI; 2003-018913/01 P-PSDB; AAE29096.	/01.		
8 E E E !	New isolated human Ras-like treating or preventing infla proliferation and apoptosis,	Ras-like ing infla poptosis,	in poly on and AIDS,	protein polypeptide, useful for diagnosing, ummation and disorders associated with cell e.g. AIDS, cancer, allergies, anemia, asthma
ξX	or stroke.	74-81. 82mm. English	ء.	
2 25	The invention re	or, capp, mights	۵-] نائد	nrotein and its corresponding
, c	nucleic acid. Th	like.	n and I	the developmen
ដុម្ព	of human therapeutics diagnosis, prevention	and	ric com nt of i	diagnostic compositions. They are useful in the treatment of inflammation and disorders.
ຸບຸ	infections or ge	with cell proliferation and or genetic immunodeficiencie	iencie	proposition of the control of the co
ប្តប្អ	Alzheimer's dise ischaemic injuri	ase, Parkinson's es e.g. myocardia	disease 1 infa	Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia, ischaemic iniuries e.g. myocardial infarction, stroke or reperfusion
ပ္ပင္	injury, toxin-in	duced diseases su	ch as c	ilcohol-induced liver damage or
بي ڊ	associated with	inflammation incl	. iney uding a	3
ប្តប្	atherosclerosis, Grave's disease.	asthma, anaemia,	Crohn'	atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus, Grave's disease, glomernlonephritis, gout, irritable bowel syndrome,
200	lupus erythemato	sus, multiple scl	erosis,	osteoarthritis, pancreatitis,
200	uveitis, trauma,	aucoimmune cnyrolairis, ineumatola archiilis, sjogiem s uveitis, trauma, or viral, bacterial, fungal, parasitic	ial, fu	6

helminthic infections. The antibodies of the invention are useful in pharmacogenomic analysis or for tissue typing. The transgenic animals are useful for studying the function of a Ras-like protein, and identifying and evaluating modulators of its activity, Ras-like protein is used in drug screening assays and its DNA is used in gene therapy. The present sequence is human Ras-like protein encoding gene. This gene is located at

Sequence 28770 BP; 6592 A; 7315 C; 7655 G; 7208 T; 0 U; 0 Other;

532 TGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCAC = = -473

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Gaps

28770; ;

Length 34; Indels 7; DB

26641 26701 26581 25861 26101 26401 26461 25801 26041 1132 26341 1372 1492 1552 1612 25741 1072 712 772 892 952 832 ACTGTCTCACCATCCCGCACCCACACAACAACAGGCCAGGCTGGAGTCCAGGCCACTTTC CCGTGTGTCCTGCTGTGCAGCTCGCTCTTTCCTTCCTAGCTATCCAAGGGGAT CGTGGGTGGGCCAAAGGCTACATCTTCCTCTTCCCCACCCCCACCCCTCTC ATGTGCCATGGCCTGCCTCCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGA AACAGCAACCGGGGAGTCCTCGAGCCTGGGGTGCCCTACCTCTACCCGTTCCCCGACCA AACGGCAACCAGGGAGTCCTCGAGCCTGGGCTGCCCTACCTCTACCCATTCCCCGACCA GAGCITTGCCCTTGCTTGGCTGCCCGCCTCTTTGGGAAACTGAGCTCAGAGGCAGG GAGCTTTGCCCTTGCTTGCCTGCCTGCCTCTTTGGGAACTGAGCTCAGAGGCAGG GCGTCTGACAGAGCTGCTGCTGCTGCCCCATAGGAAGGTGGAAGGCTTGGAAGGCCTCCGGATGCG AGCGAACTCTTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGCACCCCCACACGACACC CCTCTTCCCTCAGAAGCCCGTGGGCAGACAGGGAGCCGGGGCTTTGCCCTGCTGT CCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGCTTTGCCCCTGCTGT GAGCGGCTCTGCTGTCATCTCAAGCAGCCCTGTCCCCAGCCCGTCCACCCTGGAGTGGT GAGCGCTCTGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCTGGAGTGGT CTTCTTCAGCCTGTTTCCCCCAGCCACAGCCTCGCTACGACCCCCCACGATGTGCCGCAAGC ACTGTCTCACCATCCCGCACCCAGACAACAGCCAGGGCTGGAGTCCAGGCCACTTTC TCTTTCTCTGACCCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAACCCCGTCCC CCGIGIGICATORICAGES CAGES GGACCCAGGCTCGTGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCTGCCT GGACCCCAGGCTCGTGGGGGGGGGGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCCT CGTGGGTGGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCACCCCCATGTCCTC ATGTGCCATGGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGA TGCTTCAGAGAAAGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCT TGCTTCAGAGAAGGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCT CTICITCAGCCTGTTTCCCCCAGCCACAGGCTGCTACGACCCCCCACGATGTGCCGCAAGC TGCCAGCAATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGAGGCAAACCCCGAGGCCC 26522 26642 1013 1073 1133 1193 1253 1313 1373 1433 1493 1553 593 713 26222 653 25802 773 25862 833 25922 893 25982 953 26042 26102 26162 26282 26342 26402 26462 25682 25742 8 8 8686 6 6 6 6 6 6 6 6 6 6 셤 8 8 8 6 6 6 - A g ઠે g Š g ò 셤

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                                                                                                                                                                                                                                                               AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; noctropic; neuroprotective; osteopathic;
anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolytic; cagulant; vasotropic; antidabetic; hypotensive;
dermatological; immunosuppressive; antithyroid; and antianaemic. The
antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
sequences can be used for determining the presence of or predisposition
to, or preventing or treating pathological conditions associated with an
CORFX-associated disorder. The nucleic acids can be used to express ORFX
proteins in gene therapy vectors. The proteins and nucleic acids may be
used to treat cancers, proliferative disorders, neurodegenerative
disorders, osteoarthritis, graft va host disease, cardiovascular disease,
diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
continued setring of the proteins and immunodeficiency
(SCID), AIDS, viral, bacterial por fungal infection, malaria, autoimmune
contents asthma, allergies, aplastic anaemia, burns, wounds, bone and
cartilage damage, nocturnal haemoglobinuria, antinifiammatory disease; to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                              Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                      Claim 5; Page 1978-1979; 5507pp; English
30-MAR-2000; 2000US-00540763
                                                                        Shimkets RA, Leach
                                                                                                          WPI; 2000-602362/57.
                                                                                                                           P-PSDB; AAB41604
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CGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA 227 241 287 301 347 421 107 121 167 181 361 407 GGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGG 467 gecederacedecedecagriceedecedecedecedecederargedayagay GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG GCAGGAGAGATACCCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTT GCCCGCTGCCCGCCCGCAGTTCCCGGCCCCCGCTGGCCCCCAGTCATGGCGGAAGCAGTACGA CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA GATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG 242 GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTT GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT GGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA 18; Gaps Score 1568.2; DB 3; Length 1666; Pred. No. 0; 0; Mismatches 3; Indels 18; Sequence 1666 BP; 333 A; 529 C; 461 G; 341 T; 0 U; 2 Other; Query Match
Best Local Similarity 98.7%;
Matches 1598; Conservative C 62 801 122 168 182 228 288 302 348 362

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1063 1127 1123 1187 1303 1423 1483 1007 1067 1183 1307 1363 1427 1487 1547 1548 GGAGGCAGCTGCTTCAGAGAAAGGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCT 1607 1003 Accendentedragacica Addented additional and a second contract and a second and a second and a second a 703 767 763 827 887 883 947 943 583 647 643 707 823 GCCACTTTCAGCTGCTCCTTTCTCCGTGCATCGTGTCTCTTCTCTGCTTTTTCTCTCTTCTTCT CTGTCCCTCATGTGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGG TAGGAGGAAAACGGCAACCAGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCTTT TGGCCCTGAGAGCGGCTCTGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCC GCCGCAAGCACTGTCTCACCATCCCGCACCCACCAGACAACAGCCAGGGCTGGAGTCCAG GCGGAAGCACTGTCTCACCATCCCGCACCACCAGACAACAGCCAGGGCTGGAGTCCAG cccacricirricirgaccccrcccrccgrccricgrarcaaagcrccrcaaa ccccarcccccargreric residencia de la contra c caaddegarccaddecredregdagdriceaecerregarceagdaaddaaceree CTGTCCCTCATGTGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGG 1484 AGAGGCAGGTGCTTCAGAGAAGGAAACAAATGAGGGGTGGCAGGGATAAAAAGTCACCT GAAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATAAAGA Greatreacecercidacadaderiderecededececaradoaageaderedaageer CCGGATGCGTGCCAGCAATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGAGGAGGCAAACC CGAGGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGCACCCCA ceaececcaeceaactriceaaaaccrecrecrescreagecrererererererererere CACGACACCCCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGGCTTTGCCC TGCTGCTGTCTCTCGTGTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCCTGCC TGCTGCTGTCTCTCGTGTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCCTGCC TGGCCCTGAGAGCGGCTCTGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCC TGGAGTGGTCTTCTTCAGCCTGTTTCCCCAGCCAGGCCTGCTACGACCCCCCACGATGT CCCCACTTCTCTTTCTCTGACCCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAA CAAGGGGATGGACCCAGGCTCGTGGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCC ACCCTGCCTCGTGGGTGGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCCACCCCCA TAGGAGGGAAACAGCAACCGGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCCATT 1008 1004 1068 1064 1128 1124 1188 1248 1244 1308 1368 1364 1428 1424 1488 528 524 588 584 648 708 704 168 764 828 824 888 884 948 944 1184 1304 ઠે g g 8 8 8 g à g & g . 강 음 ò - 8 8 8 8

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1608 CCATTCTCTACCTCCCATGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATT 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
                                                                                                                                                                                                                                                                      Human, ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP1181; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match Best Local Similarity 75.8%; Score 1192.8; DB 6; Length 7924; Best Local Similarity 75.8%; Pred. No. 2.1e-279; Matches 1476; Conservative 0; Mismatches 472; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U; 0 Other;
                                                                                                                                                                                                                                   Human chemically pretreated gene sequence #76 strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7924 BP; 2087 A; 83 C; 2037 G; 3717 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 151; 24pp; English
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                                                                                                                  ВР
                                                                                                                ABK40069 standard; DNA; 7924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                             WO200202806-A2
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GGGTAAGGAGAGTTTTGGGGGTTAGTGTTTTGTTAGGTTAATTATGTATTTTATAAAGGG
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                                                                                              1336 AGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAACAGCAACCGGGGAGTCCTCGA
                                                                                                                        121 GTTTGGGGTTGTTTTATTTTATTTTTCGATTAGAGTTTTGTTTTGTTTTGGTTGT
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma an macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                        antiinflammatory, cancer, eye disease, arteriosclerosis, anaemia, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis, bowel disease, gene,
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       antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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Pred. No. 2.1e-279;
0; Mismatches 472; Indels
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01-SEP-2000; 2000DE-01043826.
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Matches 1476, Conservative
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                                                                        CTCCTGACTTACCAAAACAGGAAAACAGCAGGAGGAGGGGGCGCTCAGGACTTAGGGACAGG
                                                                                                                                                                      GTATAGCTTAGATGGTGGAAAGCAAAGGAGGAGCAGAAGTTGTAAATCACTGGCTAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
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                                     1621 ATGATTGGGAAAAGGTATGGGAGTAGAAGGAGAATTGGGATTTTAGGGTGTAGTTACGTT
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CC (NM 002538), TXNRD1 (NM 003330), UGT8 (NM 003360), MRP (NM 004956, NM 019900, NM_019901, NM_019902, NM_019862, NM 019898, NM 019899) and their complementary sequences, or a sequence (S1) chosen From 87 sequences and their complements. The chemical pretreatment is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. The office of treatment to convert cytosines (but not methyl-cytosines) into uracils. The office of treatment to convert cytosines (but not methyl-cytosines) into uracils. The office of treatment to convert cytosines (II) in particular an oligoment or a chemically pretreated by particular an oligoment or a chemically pretreated DNA of genes associated with characogenomics and their complements, arranged in an array for analysing diseases associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA continuous and cancer. The present sequence represents one the 87 DNA continuous problements in useful for diagnosis and therapy of solid continuous problement directly from WIPO at a continuous continuous directly from WIPO at continuous continuous directly from WIPO at continuous con
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Sequence 7924 BP; 1973 A; 83 C; 1827 G; 4041 T; 0 U; 0 Other;	Query Match 35.6%; Score 1160.8; DB 6; Length 7924; Best Local Similarity 74.1%; Pred. No. 1.3e-271; Matches 1468; Conservative 0; Mismatches 512; Indels 0; Gaps	TGCTTCTTCCTCTTCCCCCACCCCACTGTCCCTCATGTGCCATGGGCCTGCCT	tgacctgcgaaagtggagcatcgaggtaggagggaaacagcaaccgggggtgtctcgagc 	CIGGGGCTGCCCTACCTCTACCCATCCCCGACCAGAGCTTTGCCCTTGCCTGGCCCCTACTTGCCTGCC	GCCTGCCTCTTTGGGGAACTGAGCTCAGAGGGGGGTGCTTCAGAGAAGAAAAAGAATGA 	GGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCTACCTCCCATGCAGCATGAACACAAA AAAATAACAAAAAAAAAA	TICTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCAAGGCCTGTGGGTACTCCAGGG 	gcaaggagagccttggggtgagagagtgaggccaaccatgcactccacaaagggggggg	GCATITGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGAGCAAGGGAGAGCTGGCC 	agggacagcagtttgcacagcagagggaatgtagcaacagcagggcctcctaggccccca 	TCTTCCATTTCTTAGGTAAGAGGGTTTCCTCAGACTCCCAGGGGGGGG	agccitcagcaaccaaggiiciccigggacccaaagiitaiggagagaaggggaaagacii 	CATGGGAAGAGAAGAAGGCCCTGGGTAGAAACGCTTGGTGCTGTTCTCTTTGGCCTT
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2058	actgrggctacaggrggagggaagagctccttcctccagagtgctatgttcaggaagt 2117
2118	TTCTTTAACCCCATATGGCCCAAGAGTAGCTCGTAGGAGGCCCTTTAAAGACGGAACAG 2177
2178	TAATTTACCAGTTCTACTGGGGTTCCTGCCCACGTCCCAAGGTGGGCGAGGCCTAGGAA 2237
2238	
2298	TGGGTGTTGAGTATTCATCAACTAAGAACCAAATTCCAGGGCACTCATATGTGAAGGATA 2357
2358	AGAACCTCACTTTCCTTACTCCTCCAAAAGAAGTGGGGGAAAGAACCATCAAACCTTTCCT 2417
2418	CCTGACTTACCAAACCAGGAAAAACAGCAGGAGGGGGGCCCTCAGGACTTAGGGACAGGGT 2477
2478	atagcitagatgctggaaagcaaaggaggggggagctggtaaatcactggctaatgaga 2537
2538	AAAGGAGACAGCTAACTCTAGGATGAAGCTGTGACTAGGCTGGAGTTGCTTGAAGA 2597
2598	TGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGGCTAGGGAAGTAGGTGA 2657
2658	TGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATATTGGGCAGTGGCTC 2717
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2838	GGAAGGGAAAACATGGAATCTGTATAGACTGATAGGCCCTATCCACAGGGCCAT 2897
2898	
2958	CCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACTGTTAAGCAGGCTCTGC 3017
3018	12

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, nevosacular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                TATCTCGAATCCATATATAAATTATAAACAAAATTCATCTATTTTAAACACAAATATTTA
                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic; antianaemic; cytostatic; nootropic; neuroprotective; antianaemic; cytostatic; nootropic; natiarhemic; antiarhemic) antiarhemic; antiarhemic; antiarhemic; antiarhemic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease.
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chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.
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PR 09-DEC-2000; 2000UG-0251990P.
PR 08-DEC-2000; 2000UG-025497P.
PR 05-JAN-2001; 2001UG-025497P.
PR 05-JAN-2001; 2001UG-025497P.
PR 05-JAN-2001; 2001UG-025497P.
PA (HUMA-) HUMAN GENOME SCI INC.
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Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune prognosing disorders related to the proteins, including cancers, immune prognosing disorders related to the proteins, including and/or prognosing disorders [II]. [II] and the antibody to [I] are useful for disorders and neuronal disorders because including immune system oplymucleotides [II]. [II] and the antibody to [I] are useful for prognosing preventing and treating diseases including immune system (approxing preventing and treating diseases including immune system disorders [e.g. remained and acquired immunodeficiencies, autoimmune cc disorders [e.g. remained and acquired immunodeficiencies, and contents of each propriet of the propr

Query Match 35.6%; Score 1160.6; DB 4; Length 2021; Best Local Similarity 99.2%; Pred. No. 7.9e-272; Matches 1166; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

217 277 301 337 361 421 157 122 CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA 181 182 GATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG 241 GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT 397 61 38 ecceleracionecentricidadecentracidadecentracidades 37 GCAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTT GGTCTATGACATTAGCAGCGACCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT GCCCGCTGCCCGCCCCCCCCCCCCCCCCCCCCCCAGTCATGGCGAAGCAGTACGA GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTT GGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA ~ 62 158 242 278 302 338 398 362 셤 g à 셤 à à ద ò 용 ò ò 셤 ò

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New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's
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28-JUN-2000; 2000US-0216647P.
28-JUL-2000; 2000US-021688P.
11-JUL-2000; 2000US-021688P.
11-JUL-2000; 2000US-021748P.
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14-JUL-2000; 2000US-021748P.
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14-JUG-2000; 2000US-02255P.
14-JUG-2000; 2000US-02259P.
15-SEP-2000; 2000US-0229P.
15-SEP-2000; 2000US-0229P.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the condition based on the presence or absolute the binding partner to binding partner and determining whether the binding partner ceffects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or acid encoding the pulpeptide is useful for preventing, treating the condition or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, which involves determining the presence or absence of a mutation in The nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility or autoimmune disease, Parkinson's disease, altherosclerosis, haemophilia, thrombocytopenia. The polypeptide, the nucleic acid and the antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunosuppressive agents. The present sequence represents colly encoding a novel human protein. Note:

The sequence data for this patent did not form part of the printed sequence higher and the sequence high and the angle of this patent did not form at the patent did not form the patent direct from U
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Score 1160.6; DB 9; Length 2021;
Pred. No. 7.9e-272;
0; Mismatches 9; Indels 0;
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Query Match
Best Local Similarity 99.2
Matches 1166; Conservative
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Wehrman T;
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                                                                                                   The invention relates to an isolated polynuclectide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral calerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                      New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autolmmune disorders, multiple
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                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                             Score 1000.2; DB 6; Length 1054;
Pred. No. 6.5e-233;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                       Sequence 1054 BP; 240 A; 314 C; 304 G; 195 T; 0 U; 1 Other;
                                                                                Claim 22; SEQ ID NO 74; 284pp + Sequence Listing; English.
                                                          sclerosis, diabetes and allergies.
                                                                                                                                                                                                                                                                                                              30.7%;
99.6%;
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Best Local Similarity 99.6
Matches 1002; Conservative
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This invention describes novel polypeptide fragments (I) and the polynucleotides (II) that encode them that are highly expressed in a human bladder tumour and which have cytostatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for treatment of bladder cancer, to directly treat this form of cancer (including expression from gene therapy vectors) or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling BSTs (expressed sequence tags) from a particular issue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures associated with the fact that ESTs from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATCCCGCACCCACCAGACAACAGCCAGGCTGGAGTCCAGGCCA 1043
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                                                                                                                                                                                                      73
            gene, distorting the estimated frequency of occurrence in a particular tissue. AAZ43260-Z43309 represent expressed sequence tag (BST) fragment isolated from a human bladder tumour cDNA library which encode the proteins represented in AAY66143-Y66198
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different libraries may represent different parts of the same unknown
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                                                                                                                 Length 895;
                                                                                   Sequence 895 BP; 249 A; 205 C; 228 G; 213 T; 0 U; 0 Other;
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99.5%; Pred. No. 2.4e-200;
live 0; Mismatches 3;
                                                                                                                             Best Local Similarity 99.5
Matches 879; Conservative
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antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; rheumatoid arthritis; inflammatory condition; sickle call anaemia; hyperproinfection; hepatitis C; blood disorder; sickle call anaemia; hyperproinferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; cardicovascular; respiratory; bown syndrome; ischaemia; renal disorder; cardicovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; ss;
                                                                                                                                                                                                                                                                               Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
                                                                                                                                                                                                                          cDNA encoding novel signal transduction pathway protein, Seq ID 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acquired immune deficiency syndrome
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04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
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19-AAY-2000; 2000US-0198123F.
28-JUN-2000; 2000US-0214886F.
28-JUN-2000; 2000US-0214886F.
30-JUN-2000; 2000US-0214886F.
07-JUL-2000; 2000US-0216647F.
07-JUL-2000; 2000US-0216890F.
11-JUL-2000; 2000US-021890F.
11-JUL-2000; 2000US-021890F.
26-JUL-2000; 2000US-021890F.
26-JUL-2000; 2000US-0224518F.
14-AUG-2000; 2000US-0224518F.
14-AUG-2000; 2000US-022513F.
14-AUG-2000; 2000US-0225213F.
14-AUG-2000; 2000US-022526F.
14-AUG-2000; 2000US-022526F.
14-AUG-2000; 2000US-022526F.
                                                  AAS27472 standard; cDNA; 566
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                                                                                                                                                                  (first entry)
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06-SEP-2000;
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22-AUG-2000;
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14-AUG-2000;
18-AUG-2000;
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RESULT 13
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2000US-0231413P
2000US-0231414P
2000US-0232080P
2000US-0231968P
2000US-0231968P
2000US-023239P
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2000US-0249209P.
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PR 17-NOV-2000; 200008-029245P.
PR 17-NOV-2000; 200008-029245P.
PR 17-NOV-2000; 200008-029265P.
PR 17-NOV-2000; 200008-02929P.
PR 17-NOV-2000; 200008-02929P.
PR 17-NOV-2000; 200008-02929P.
PR 17-NOV-2000; 200008-02929P.
PR 17-NOV-2000; 200008-02920P.
PR 17-NOV-2000; 200008-02920P.
PR 17-NOV-2000; 200008-02920P.
PR 17-NOV-2000; 200008-02920P.
PR 01-DEC-2000; 200008-02920P.
PR 01-DEC-20009-02920P.
PR 01-
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16.4%; Score 534.2; DB 4; Length 566; 98.9%; Pred. No. 1.2e-119; tive 2; Mismatches 4; Indels 0

Best Local Similarity 98.9 Matches 533; Conservative

Query Match

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TGTGCTGTTCCGGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCTGTG 121

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se; gene; human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; fimunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration.
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2000US-0180628P.
2000US-021664PP.
2000US-021688P.
2000US-0217487P.
2000US-0217487P.
2000US-0217496P.
2000US-0220963P.
2000US-0220964P.
2000US-0220964P.
2000US-022564P.
2000US-022567P.
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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the polypeptide is also useful for identifying a binding partner to the polypeptide which involves contacting the polypeptide of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid a pathological condition or a susceptibility to a pathological condition in a subject, which involves determining the pathological condition or a susceptibility to a pathological condition or disease, atherosclerosis, haemophila, thrombocytopenia. The polypeptide, the nucleic acid and an antibody to the polypeptide are useful for treating autoimmune disease, Parkinson's disease, silicosis, gastrointestinal cathand and an antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce higher as adjuvants to enhance immune responses, and as agents to induce higher as present sequence data for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at sequence that for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's
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02-OCT-2000; 2000US-0237037P.

02-OCT-2000; 2000US-0237038P.

02-OCT-2000; 2000US-0237039P.

13-OCT-2000; 2000US-0237040P.

13-OCT-2000; 2000US-02499P.

20-OCT-2000; 2000US-0241809P.

01-NOV-2000; 2000US-0241809P.

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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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05-SBP-2000;
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                                                                                                                                CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA
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                                                     GCCCGCTGCCCGCCCGCAGTTCCCCGGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGA
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Length 566;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding colon tumour protein, SEQ ID No 303
 16.4%; Score 534.2; DB 9; 98.9%; Pred. No. 1.2e-119;
               Pred. No. 1.26
2; Mismatches
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28-MAR-2001; 2001US-0279763P.
29-JUN-2001; 2001US-0302051P.
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                                                                                                       The invention relates to polynuclectides encoding colon tumour proteins. The polynuclectides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of Colon cancer. Polynuclectide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer. ABK44450-ABK46237 represent. Coding sequences of human colon tumour proteins of the invention. Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTA 2701
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for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer.
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                                                                    Claim 1; SEQ ID NO 303; 147pp; English.
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Sequence 1161, Ap Sequence 7460, Ap Sequence 112, Appl Sequence 112, Appl Sequence 1124, Appl Sequence 1124, Appl Sequence 6, Appli Sequence 11, Appl Sequence 11, Appl Sequence 17, Appl Sequence 2, Appli Sequence 2, Appli Sequence 1159, Ap Sequence 15288, Ap Sequence 15288, Ap Sequence 15288, Appli Sequence 15288, Ap Sequence 15288, Appli Sequence 15288, Ap Sequence 15288, Ap Sequence 15288, Appli Sequence 15288, A	Acid Targets and Methods of	; Length 730; ; Indels 3; Gaps 1	crecceccecagrateccegeccegergeccagreargecgaagcagracaargee 66	rgitcggctgctgctgatcgggactccgggtgggcaagacctgcctg	TCACCGACAACGAGTTCCACCTCGCACATCTCCACCATCGGTGTTGACTTTAAGATGA 186
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                                                                                                           344 Accacción accaca de contra de
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPUTER: 
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Patent No. 5843717

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Guegler, Karl

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSES:

ADDRESSES:

CITY: Palo Alto
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCHOOKET NUMBER: PF-
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1340 base pairs
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STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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CLONE: 738957
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IMMEDIATE SOURCE:
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Query Match

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382 GACTCTGCCCATGAGCGTGTGGTGAAGAGGAGGACGGGGAGAAGCTGGCCAAGGAGTAT 441
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Pred. No. 3e-31;
0; Mismatches 209; Indels
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COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTE: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESG for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/198,184
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APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0240 US
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
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; Sequence 2, Application US/09198184
; Patent No. 6010859
; GENERAL INFORMATION:
        al Similarity 59.0%;
305; Conservative
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Matches 305; Conserv
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357 AACGTGAAGCAGTGGCAGGAGATTGACCGCTATGCCAGCGAGAACGTCAATAAGCTC 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.8%; Score 156; DB 2; Length 925; 56.7%; Pred. No. 3.5e-31; tive 0; Mismatches 220; Indels
                        CURRENTING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: FAILEd Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 ATTAAAGAGTCATTCACGCGTCTGACAG 543
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                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REFERENCE DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/09154602; Patent No. 6300472
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   Diskette
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STRANDEDNESS: single
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IMMEDIATE SOURCE:
   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGGTGCGATTCAAGGATGGTGCTTTCCTGGCGGGGACCTTCATCTCCACCGTAGCATT 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 GACTCTGCCCATGAGCGTGTGGTGAAGAGGGAGGACGGGGAGAAGCTGGCCAAGGAGTAT 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 209; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 156.6; DB 3;
Pred. No. 3e-31;
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APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08916901 Patent No. 5892012 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        4.8%;
                            TELEFAX: 415-845-4166
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1340 base pairs
415-855-0555
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Best Local Similarity 59.0°
Matches 305; Conservative
                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                   TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCNOTO4
CLONE: 738957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3047 ACTTGTCCTTCATCGAGACCTCAGCCTTGGATTCCACTAACGTAGAGGAAGCATTCAAG 3105
417 CTGGTGGCCAACAAGAGCGACCTCACCACCAAGAAGGTGGTGGACAACACCCACAGGCCAAG 476
                                                                                               477 GAGTTTGCAGACTCTCTGGGCATCCCCTTCTTGGAGACGAGCGCCCAAGAATGCCACCAAT 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2627 AGTACGACTACCTATICAAAGTGGTGCTCATCGGGGACTCAGGCGTGGGCAAGAGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 ACTITAAGAIGAAGACCAIAGAGGIAGACGGCAICAAAGIGCGGAIACAGAICTGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2747 AGTTCGCCACCCGCAGCATCCAGGTGGACGGCAAGACCATCAAGGCGCAGATCTGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 144.6; DB 4; Length
Pred. No. 8.1e-28;
0; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature

CTHER INFORMATION: Incyte ID No. 6673545 1088524.8

NAME/KEY: unsure

LOCATION: 2060-2170, 3796, 3799, 3816

US-09-919-172-49
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                   516 ATTAAAGAGTCATTCACGCGTCTGACAG 543
                                                                                                                                                                                               537 grcgagcaggcaricardaccardgcrd 564
                                                                                                                                                                                                                                                                                              US-09-919-172-49
US-09-919-172-49
; Sequence 49, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.4%;
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 49
LENGTH: 3936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 ATCTCCACCATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 Arcagcaccarceacegeresacrircassarcesaccarceaseresearescaaaacrare 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 AAACTICAGATCIGGGACACAGGGGCCAGGAACGGTICGGGACGATCACTICCAGCIAC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 AACGTGAAGCAGTGGCTGCAGGAGATTGACCGCTATGCCAGCGAGAACGTCAATAAGCTC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTATTGGGAATAAGGCTGATGAGGAGCAGAAACGGCAGGTGGGAAGAGGAGCAAGGGCAG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 raccesesescrearescarcaresregierarianeaescareaecaeseaeresrecraeses 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCGCCCCATGAACCCCCGAATATGACTACCTGTTTAAGCTGCTTTTGATTGGCGACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCCAGTCATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGTGGGCAAGTCATGCCTGCTCCTGCGGTTTGCTGATGACACGTACACAGAGAGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 CGGATACAGATCTGGGACACTGCAGGGCAGAGAGATACCAGACCATCACAAAGCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACATCATGAAGTGGGTCAGTGACGTGGATGAGTACGCACCAGAAGGCGTCCAGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.8%; Score 156; DB 4; Length 925;
Best Local Similarity 56.7%; Pred. No. 3.5e-31;
Matches 288; Conservative 0; Mismatches 220; Indels
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
                                                                                                                                                                                                    3: Incyte Pharmaceuticals, Inc
3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMUNICATION INFORMATION:
TELEPAN: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
  APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incvr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: LIVRTUTO4
CLONE: 2514506
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                                                                                                                                                                                                                      STREET: 3174 POI
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                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                           94304
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119 GGGTGATGCTTCTTGGAGANTCGGGCGTCGGCAAAACCTGTTTCCTGATCCAATTCAAG 178
                                                                                                                                 133 ACAACGAGTTCCACTCCT---CGCACATCTCCACCATCGGTGTTGACTTTAAGATGAAGA 189
                                                                                                                                                                                         179 ACGGGCCTTCCTGTCCGGAACCTTNATAGCCACCGTCGGCATAGACTTCAGGAATAAG 238
                                                                                                                                                                                                                                                                  190 CCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGGGCAGGAGA 249
                                                                                                                                                                                                                                                                                                                                                                                                       GATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTTGGTCTATG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGTGGATGAGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 ATGCCCAGAGGACGTGGTTATGCTTCTAGGCAACAGGCCGATGTAAGCAGCGAAA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCAGGTGGGAAGAGGACAAGGGCAGCTGGCGAAGGAGTATGGCATGGACTTCTATG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 GGGTGATCCGTTCTGAAGATGGAGAGACACTCGCCCAGGGAATATGGTGTTCCTTTCATGG 538
239 TGGTGACAGTGGATGGTTCCAGGGTGAAGCTTCAGATCTGGGACACTGCAGGACACAGGAGC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 ACATCACCAACCAGTCCTCTTTGACAACATCAGGGCCTGGCTCACAGAGATTCATGAGT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGAGCAGAAAC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 AAACAAGIGCCIGCACCAACCICAACAITAAAGAGICAIT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  539 AGACCAGTGCCAAGACTGCCATGAACGTGGAGTTGGCCTT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPES: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
'APPLICATION NUMBER: US/09/075,454
PTI,ING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cerrone, Michael C.
REGIGTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Nail C.
APPLICANT: Patterson, Chandra
APPLICANT: Batra, Sajeev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
FILING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09075454 Patent No. 6391580
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ADDRESSEE: INCYTE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (12)
OTHER INFORMATION: The n at position 12 represents an unknown.
NAME/KEY: unsure.
LOCATION: (14)...(15)
OTHER INFORMATION: The n at positions 14 through 15 represents an OTHER INFORMATION: unknown.
NAME/KEY: unsure.
LOCATION: (17)...(18)
OTHER INFORMATION: The n at positions 17 through 18 represents an OTHER INFORMATION: unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (3)
OTHER INFORMATION: The n at position 3 represents an unknown.
NAME/KEY: unsure
LOCATION: (6).(8)
OTHER INFORMATION: The n at positions 6 through 8 represents an OTHER INFORMATION: unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ب
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OTHER INFORMATION: The n at position 108 represents an unknown.
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (726)
OTHER INFORMATION: The n at position 726 represents an unknown.

    LOCATION: (204)
    OTHER INFORMATION: The n at position 204 represents an unknown.
US-09-255-920A-6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: The n at position 138 represents an unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (22)
OTHER INFORMATION: The n at position 22 represents an unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (25)
OTHER INFORMATION: The n at position 25 represents an unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.2%; Score 138; DB 4; Length 842; Best Local Similarity 57.6%; Pred. No. 1.9e-26; Matches 265; Conservative 0; Mismatches 192; Indels
                                                                                                                                                             | GREAT | FO. 66243980 |
| GENERAL INCOMMATION: |
| GAPLICANT: Fisher, Joseph |
| APPLICANT: Fisher, James |
| APPLICANT: Anderson, David |
| APPLICANT: Lorens, James |
| APPLICANT: Lorens, James |
| APPLICANT: Huang, Betty |
| APPLICANT: Huang, Betty |
| APPLICANT: Shen, Mary |
| TITLE OF INVENTION: EXOL and EXO2, EXOCYTOTIC PROTEINS |
| TITLE OF INVENTION: EXOL and EXO2, EXOCYTOTIC PROTEINS |
| FILE REFERENCE: A65905-1/DJB/RMS |
| CURRENT FILING DATE: 1999-02-23 |
| PRIOR PILING DATE: 1998-02-23 |
| PRIOR FILING DATE: 1998-05-26 |
| NUMBER OF SEQ ID NOTS: 16 |
| NUMBER OF SEQ ID NOTS: 16 |
| SOFFWANDE: DATE: 1998-05-26 |
| NUMBER OF SEQ ID NOTS: 16 |
| SOFFWANDE: DATE: 1998-05-26 |
| NUMBER OF SEQ ID NOTS: 16 |
| SOFFWANDE: DATE: 1998-05-26 |
| NUMBER OF SEQ ID NOTS: 16 |
| SOFFWANDE: DATE: 1998-05-26 |
| SOFFWANDE: DATE: DATE: 1998-05-26 |
| SOFFWANDE: DATE: DA
                                                                                                                          Sequence 6, Application US/09255920A
Patent No. 6623980
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LOCATION: (823)
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SEQ ID NO 6
LENGTH: 842
                                                                                              -09-255-920A-6
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234 ACTGCAGGGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGG 293
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Pred. No. 6.5e-26;
0; Mismatches 193; Indels
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APPLICANT: Jones, Karen A.
APPLICANT: Walker, Michael G.
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION UNMERE: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SEQ ID NO 142
LENGTH: 2612
             FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ. ID NOS: 1105
SEQ. ID NO 959
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; Patent No. 6426186
; GENERAL INFORMATION:
Polypeptides
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Best Local Similarity 57.5%;
Matches 265; Conservative
                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (124)..(699)
US-09-620-312D-959
TITLE OF INVENTION:
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Pred. No. 5.7e-26;
0; Mismatches 193; Indels
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APPLICANT: Wang, Zhiwei
APPLICANT: Ohn Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 959, Application US/09620312D Patent No. 6569662
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Best Local Similarity 57.5%;
Matches 265; Conservative
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELEFAX: 650-845-4166
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; CLONE: 1528559
US-09-075-454-10
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Ma, Yunqing
                                                                                                                                                  TOPOLOGY: linear IMMEDIATE SOURCE:
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E: INCYTE PHARMACEUTICALS, INC
3174 PORTER DRIVE
                NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 646
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                Query Match
Best Local Similarity 54.6%;
Matches 266; Conservative
PRIOR FILING DATE: 2000-01-21
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CITY: PALO ALFO
CALIFORNIA
                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (156)..(839)
US-09-620-312D-646
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                                                                                                         Length 2612;
                                                                                                         Score 136.2; DB 4; Length
Pred. No. 1.1e-25;
0; Mismatches 193; Indels
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                    ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INCRMATION: Incyte ID No. 6426186 412477.1CB1
US-09-484-970B-142
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TITLE OF INVENTION: No. 659662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CTP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
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Patent No. 6569662
GENERAL INFORMATION:
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
                                                                                                       Query Match
Best Local Similarity 57.5°
Matches 265; Conservative
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Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
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Yang, Yonghong
Wang, Jian-Rui
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
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 ORGANISM: Homo sapiens
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APPLICANT:
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APPLICANT:
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229 AGAÁCTTTGÁCTACATGTTCAAATTACŤCAŤCÁTCGGCAATAGCAGTGTGGGGGAÁAACAT 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                 289 CTTTTCTATTCCGTTATGCAGATGACTCCTTTACATCTGCATTCGTCAGCACAGTTGGGA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 TCAGTGACGTGGATGAGGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 CAACTCAAATCAAAACATACTCTTGGGACAATGCCCAAGTTATTCTGGTTGGGAACAAGT 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 ATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           649 TTGGGTTTGAGTTTTTTGAAACAAGTGCCAAGGACAATAATGTCAAGCAGACATTTG 708
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                                                                                                                                                                        52 AGCAGTACGATGTGCTGTTCCGGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCT
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jointee Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
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Length 1069;
Score 133.4; DB 4; Length
Pred. No. 3.5e-25;
0; Mismatches 221; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 AGGAATAGATCGTTATGCCAGTGAAATGTCAACAATTGTTGGTAGGGAACAAATGTG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 ATGAGGAGCAGAAACGGCAGGTGGGAAGAAGAGCAAGGGCAGCAGCTGGCGAAGGAGTATG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 TATTTTTGGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 AGTACGATGTGCTGTTCCGGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCC
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             SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 7.5e-23;
0; Mismatches 228;
                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEFAX: (550) 845-4166
INFORMATION FOR SEQ ID NO: 1422:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                               APPLICATION NUMBER: US/09/016,434
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.8%;
Best Local Similarity 53.4%;
Matches 261; Conservative
                                                                HEREWITH
                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGATGGCAG 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; CLONE: 9550059
US-09-016-434-1422
                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                       FILING DATE:
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RESULT 13 8.09-620-312D-828 ; Sequence 828, Application US/09620312D ; Patent No. 6569662

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273 AAGGTGGTGCTGATCGGCGAATCAGGTGTGGGGAAGACCAATCTACTCTCCCGATTCACG 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTGACTTTAAGATGAAGACC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 CTAACCAAGCACCAGACCTATGCTGTGGAGCGATGGCTGAAGGAGCTCTATGACCAT
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Pred. No. 1.4e-22;
0; Mismatches 284; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 828
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51.7%;
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                                                                                                                                                                                       Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
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Best Local Similarity 51.7
Matches 307; Conservative
Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang, Yonghong
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (234)..(875)
US-09-620-312D-828
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60 TGCGGANCAAGATGGGAATGGAACTGAGGAAGATTATAACTTTGTCTTCAAGGTGGTGC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 GCACCGCTGCTGTCAAGGCTCAGATCTGGGACAGCTGGCCTGGAGCGGTACCGAGCCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 TCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTTGGTCTATGACATTAGCAGCG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATCGGGGACTCCGGGGTGGGCAAGACCTGCCTGCTGTGCCGCTTCACCGACAACGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCGGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGATGTGTTCCGGCTGCTGCTGC
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Pred. No. 7.3e-22;
0; Mismatches 280; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,423
FILING DATE: Herewith
CLASSIPRICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                       APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                 3: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF-0183 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                           5-08-773-423-4
Sequence 4, Application US/08773423
Patent No. 5869291
                                                                                                                                                                                                                         Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.7%;
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TYPE: nucleic acid
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Best Local Similarity 51.5
Matches 301; Conservative
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SEQUENCE CHARACTERISTICS
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702 CGATGGCAG 710
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CLONE: Consensus
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TOPOLOGY: linea:
IMMEDIATE SOURCE:
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     ACAAGTGCCTGCACCAACCTCAACATTAA---AGAGTCATTCACGCGTCTGACAGAGCTG 548
                                                     115 TGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTACATCAGCACAATTGGTGTGG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 ACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCAGGGCAGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 TCATAGTTGTGTATGATGTGACAGATCAGGAGTCCTTCAATAATGTTAAACAGTGGCTGC 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 GTGACGTGGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 ATGAGGAGCAGAAACGGCAGGTGGGAAGAGAGAGCAAGGCAGCAGCAGCTGGCGAAGGAGTATG 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 ATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATCAAGCTTCAAATATGGGACA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402 CAGCAGGCCAGGAAAGATTTCGAACAATCACCTCCAGTTATTACAGAGGAGCCCATGGCA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATITITIGGICIATGACATTAGCAGCGAGCGCTCTIACCAGCACATCATGAAGTGGGTCA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 AGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCC
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                                                                                                              549 GTGCTGCAGGCCCATAGGAAGGAGCTGGAAGGCCTCCGGATGCGTGCCAGCAAT 602
                                                                                                                                                                753 TTTGCGAAGGTGTCCAAGCAGAGACAGAACAGCATCCGGACCAATGCCATCACT 806
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                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE FILE REFRENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6682888 411474.10
NAME/KEY: nusure
LOCATION: 3488-3788
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09566921
Patent No. 6612888
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
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ORGANISM: Homo sapiens
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SEQ ID NO 7
LENGTH: 8137
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                                                        322 AGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGTGGATGAGTACGCACCAGAAG 381
                                                                                    382 GCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGAGGAGAAACGGCAGGTGGGAA 441
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Search completed: March 21, 2004, 02:20:55 Job time : 231 secs

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Sequence 2, Appli
Sequence 2111, Ap
Sequence 151, App
Sequence 152, App
Sequence 152, App
Sequence 8, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 31, Appl
                                                                                                                                              March 21, 2004, 02:05:45; Search time 1083 Seconds (without alignments) 11124.786 Million cell updates/sec
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(cgn2_6/ptodata/2/pubpna/USO6_PUBM_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USO6_PUBM_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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(cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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9 US-09-817-198A-3

14 US-10-311-455-2111

16 US-10-257-166-151

14 US-10-257-166-152

15 US-09-26-152

17 US-00-363-616-74

18 US-09-817-198A-28

19 US-09-817-198A-29

10 US-09-817-198A-30

10 US-09-817-198A-30

10 US-09-817-198A-30

10 US-09-817-198A-31

10 US-09-817-198A-31

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10 US-09-817-198A-31

10 US-09-817-198A-31

10 US-09-817-198A-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2438257 segs, 1849576744 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA:
                                                                                                  nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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11192.8
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Perfect score:
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516.6
477.4
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	16	477.4	14.7	481	13	US-10-033-528-303 US-10-099-926-303	Sequence 303, App Sequence 303, App
	C 18	438.8	13	463	6	US-09-964-824A-26 US-09-918-995-20848	Sequence 26, Appl
	2021	306.8	9.9	310	13	US-09-878-178-1930 US-10-046-935-1930	Sequence 1930, Ap Sequence 1930, Ap
	22	306.8	9, 1,	310	14	US-10-146-502-1930 US-10-264-049-290	Sequence 1930, Ap
	C 24	221.8	. 6	358	17	US-10-240-425-504	Sequence 504, App
	797	217.8		1161	000	US-09-794-257-7 US-09-794-257-7	Sequence 7, Appli
	28	217.8	. ·	2497	ש פ	US-09-834-975-885	Sequence 875, App
	30 30	217.8		2497	o 0	US-09-834-975-894 US-09-834-975-896	Sequence 894, App Sequence 896, App
	31	210	6	601	<u>ه</u> د	US-09-817-198A-32	Sequence 32, Appl
	3 E	195.6		3164	7	US-10-925-300-631 US-10-096-534-38	Sequence 511, App Sequence 38, Appl
	34	192	ι, π	995	14	US-10-084-817-256	Sequence 256, App
	36	180	, rų	621	14,	US-10-128-714-2241	Sequence 2241, Ap
	37 38	180 174.8	v. v.	621 967	17	US-10-128-714-7600 US-10-425-114-21224	Sequence 7600, Ap Sequence 21224, A
	30	173.4	ı, ı	651	٥:	US-09-938-842A-836	Sequence 836, App
	4.4	169.8	'n'n	374	12	US-10-085-783A-56703	Sequence 56703, A
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	. 4. 4. J. 4. 7.	167	1.4.4.	968 1162	122	US-10-425-114-12529 US-10-424-599-58679	Sequence 24433, A Sequence 12529, A Sequence 58679, A
						ALIGNMENTS	
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	; Paten; GENER	It No. U	\$2002014 RMATION:	6758A1	1	; Patent No. US20020146758A1 ; BENERAL INFORMATION:	
	, APPL	ICANT:	YE, Jane	et al.	5	THAN DAG TYTE DOOMETING	
-			VENTION:	NUCLE	4 4 3 2 3	LES ENCODING	THESE HUMAN RAS-LIKE
	FILE	REFERE	NCE: CLO	PRO1E.	Š,	AND USES INEREOF	
	CURR	ENT APP	LICATION	NUMBER :	. US	/09/817,198A 27	
	NUMB	ER OF S	EQ ID NO	S: 33	3		
	; SEC I	TWARE: F. ID NO 1	astSEQ f	or Windo	SW.S	Version 4.0	
- '		TH: 32	57				
	; TYPE; ; ORGAN US-09-817	: DNA IISM: 7-198A	Human 1				
	Query Ma Best Loc Matches	y Match Local Simila hes 3257; Co	imilarity ; Conser	100.09 larity 100.09 Conservative	960	Score 3257; DB 9; Pred. No. 0; 0; Mismatches 0;	Length 3257; Indels 0; Gaps 0;
	à	-	TGCCCGCT	ນວອວວວອ	Ω.	GTTCCCGGCCCCGCTGGCCCCAGT	CATGGCGAAGCAGTACG 60
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	à	121	GCCGCTTC	ACCGACA	ACGA	GCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGTGTTGACTTTA	CATCGGTGTTGACTTTA 180
	qq	121	GCCGCTTC	ACCGACA	CGA	GTTCCACTCCTCGCACATCTCCAC	CATCGGTGTTGACTTTA 180
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1311 TGGGGCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGGGAAACAGCAA 1380 1311 TGGGGCTGCCTCCCCAGTGACCTGCGAAGTAGAGCATAGACACCAA 1380 1311 TGGGGCTGCCTCCCCAGTGACCTCTCACCCTCTCACCGACCAGAGCTTTG 1440 1311 CCGGGGAGTTCCCCAGCTGACCTCTCACCCTCTCACCCTCTCACCGACCAGAGCTTTTC 1440 1411 CCGGGGAGTTCCTCGACCTCTCACCCTCTCACCCTCTCACCGACCAGAGCTTTCA 1500 1411 CCCTTCCTTGGCTTCCCCCTCTCTCTCTCTCCTCCACGACCTTCACTCTCACCTCTCACGACCACACTTCACTCTCACAGACACACTTCACTCCCCCA 1560 1501 AGAAGGAAACAAAATTCACCTCCACTCTTTGACACACACA	
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iive 0; Mismatches
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
LENGTH: 28770
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Best Local Similarity 98.8
Matches 2717; Conservative
                                                ; TYPE: DNA
; ORGANISM: Human
US-09-817-198A-3
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              GGACTTAGGGACAGGGTATAGCTTAGATGGTGGAAAGCAAAGGAGAGCAGGAAGTTGTAA
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Patent No. US20020146758A1
GENERAL INCRMATION:
GENERAL INCRMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE ITLLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO01188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
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2513 ACTIONACTAGGACTAGGACACAGGACTACATGAGAAAGCAAAGC	RESULT 3 US-10-311-455-2111 is Sequence 2111, Application US/10311455 is Sequence 2111, Application US/10311455 is Publication No. US20030143606A1 is General Information Sequence 2111, Application No. US20030143606A1 is FIREAL INFORMATION: APPLICANT: PIEPENBROCK, Christian APPLICANT: BEALIN, Kurt ITILE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi ITILE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi FILE REPRENCE: 2013.1014 CURRENT APPLICATION NUMBER: DO7-02 PRIOR APPLICATION NUMBER: DE 100438259.7 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 2424 SEQ ID NO 2111 LENGTH: 7924
	QY 2153 GGAGGCCTTTAAAGACGAACTAATTTACCAGTTCTACTGGGGTTCCTGCCCACCG 2212 DD 27242 GGAGGCCTTTAAAGACGGAACAGTACTTACTGGGGTTCCTGCCCACCG 27301 DD 2732 TCCCAAGGTGGGAGGCTTAGTATTTCACCAGTTCTTACTGGGTTCCTGCCCACCG 2772 DD 27302 TCCCAAGGTGGCAGGCCTAGGAAGAGGGGTCATTCTTAAGCCACAATTAGCTGCACTG 2772 QY 2273 CGTGGCTGCAGCCTAGGAACAAGAAGAGGGTCATTCTTAAGCCACAATTAGCTGCACTG 27361 QY 2273 CGTGGCTGCAGCCAAACAAAGAACAAGAACAATTAGCTACCAAATTAGCTGCACTAGAAT 27361 DD 27362 GGGGCTGCAGCCAAACAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAACCAAAAT 27421 DD 27363 CGGGGCTCATATGTGAAGATAAGAACCTCACTTCCTTACTCCTCCAAAAAGAAGTG 27421 DD 27422 CCAGGGCACTCATATGTGAAGAATAAGAACCTCACTTCCTTACTCCTCCCAAAAAGAAGTG 27481 DD 27422 CCAGGGCACTCATTACTCCTCACTTCCTTACTCCTCCCAAAAAGAAGG 27481 DD 27482 GGGAAAGAACATTCCTCCTGACTTACCAAACCAGGAAAAGAGGGAGAGG 2751 CT482 GGGAAAGAACATCAAACCTTCCTCTCATACCAACAGGAGAAGGGAGAGG 2751 CAGGAAAGAACAACATCCTCCTGACTTACCAAACCAGGAAAAGAGAGAG

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Meth
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Meth
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the CURRENT PILL OF INVENTION: MABER: US/10/257,166
CURRENT APPLICATION NUMBER: US/10/257,166
CURRENT APPLICATION NUMBER: PCT/EP01/07470
DE 10032529-7
PRIOR FILLING DATE: 2001-06-29
2000-06-30
2000-06-30
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                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 151
LENGTH: 7924
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	TITLE OF INVENTION: OBJOINT SET OF USE OF US

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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
(MS-10-257-166-152
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
FILE REFERENCE: 5013.1011
CURRENT APPLICATION NUMBER: US/10/257,166
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: PCT/EP01/07470
DE 10043826.1
DE 10043826.1
PRIOR FILING DATE: 2001-06-29
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Publication No. US20040023230A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 178
SEQ ID NO 152
LENGTH: 7924
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US-10-257-166-152/c
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Length 2021;

DB 9;

35.6%; Score 1160.6;

Query Match

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                                                                                                                                                                                                                                                      CAATCTATAAACCAATATTTCAACTTTCCCTAAAAATCAAACAAAATACCATTCATTATC 6423
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ATAGCTTAGATGGTGGAAAGCAAAGGAGAGCAGGAAGTTGTAAATCACTGGCTAATGAGA
                                                           2538 AAAGGAGACAGCTAACTCTAGGATGAAGCTGTGACTAGGCTGGAGTTGCTTTGAAGA
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RESULT 7
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Sequence 88, Application US/09764868
Fatent No. US20020168711A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION UNMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
FILO EXPLICATION OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
LENGTH: 2021
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-868-88
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	Query Match Best Local Si Matches 1166;	35.6*; SCOZE 1100.0; UB 9; Lengun 2021; milarity 99.2*; Pred. No. 1.2e-309; ; Conservative 0; Mismatches 9; Indels 0; Gaps
õ		GCCCGCTGCCCCCCCGCAGTTCCCGGCCCCGCTGGCCCAGTCATGGCGAAGCAGTACGA 61
g	38	sacracicecededagricecededececeradececagricarádecedadeda 9
8 8	62 98	TGTGCTGTTCCGGCTGCTGTTCGGGGACTCCGGGGTGGGCAAGACCTGCCTG
ð		TTCACCGACAACGAGTTCCACTCCTCGCACTCTCCACCGTGTTGACTTTAA 1
면	0 158	TITCACCGACAACGAGIICCACTCCTCGCACAICICCACCAICGGIGIIG
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ò	Ä	GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTT 301
점	278	gcaggadadataccadccatcacaaagcagtactatcggcgggcccaggggatatttt 337
ð	m	GGTCTATGACATTAGCAGCGCTCTTACCAGCACATCATGAAGTGGGGTCAGTGACGT 361
셤	338	GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGGTCAGTGACGT 397
à	, 362	AGAAGATCCTTATTGGAATAAGGCTGATGAGGA 4
g	398	GGATGAGTACGCACCAGAAGGCCCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA 457
ò	422	GCAGAAACGCAGCTGGGAAGAGAGAGAGCACCAGCTGGCGAAGGAGTATGGCATGGA 481
g	0 458	CATGGA 5
δ	482	CITCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCACGCGTCTGAC 541
යි	518	CTTCTATGAAACAAGTGCCTGCACCTCAACATTAAAGAGTCATTCACGCGTCTGAC 577
ð	, 542	AGAGCTCGTGCTGCAGGCCCATAGGAAGAAGCTCGAAAGGCTCCGGATGCGTCCCAGCAA 601
<u>유</u>	578	AGAGCTICGTGCTGCAGGCCCATAGGAAGGAGCTGGAAGGCCTCCGGATGCGTGCCAGCAA 637
à	, 602	TGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGAGGCAAACCCGAGGGCCCAGCGAACTC 661
<u>업</u>	5 638	
ð	, 662	TTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGGCACCCCACACGACCCCTCTTCCC 721
d	869 0	CTCTTCC
8	72	CAGGAGGCCCGTGGCCACACACGGGGCCGGGGCTTTGCCCTGCTGCTGTTCCTCTCTGTG 78
셤	5 758	CCTCI
õ	782	TGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCCTGCCTG
a	5 818	TGATGACCCTATTGAGTATCAGAAGCCACTACCCCCTGCCTG
õ	842	IGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCCTGGAGTGGTCTTCTTCAG 901
g	5 878	TGTCATCTCAAGCAGCCCCTGTTCTTCATCTAACAAGAAGTGGGCTTCTTCA
à	7 902	CCTGTTTCCCCAGCCACAGGCCTGCTACGACCCCCACGATGTGCCGCAAGCACTGTCTCA 961
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OY 482 CITCTATGAACAAGTGCCTGCACCAACTCAACATTAAAGAGTCATTCACGCGTCTGAC 541	AGAGCTGGTGCTGCAGGCCCATAGGAAGCTGGAAGGCCTCCGGATGCGTGCCAGCAA	578 AGAGCTGCTGCTGCTGCCCATAGGAAGGAGCTGGAAGGCCTCCGGATGCGTGCCAGCAA 602 TGAGTTGGCAGAGAGAGAGGAGGAGGAGGCGAAACCCGAGGGAAGCCCAAGGAACTC	Db 638 TGAGTTGGCAGTGGCAGGAGGAGGAGGAGGACCAACCCAAGCGAACTC 697	Qy 722 TCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGCTTTGCCCTGCTGCTGTGTGTG	Qy 782 TGATGACCTATTGAGTATCAGTAGCCACTACTCCCCCTGCCTG	Oy 842 TGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCTGGAGTGGTCTTCTTCAG 901	QY 902 CCTGTTTCCCCAGCCACAGGCCTGCTACCACCACCACGATGTGCCGCAAGCACTGTCTCA 961	Qy 962 CCATCCGCACCCACCAGACAACAGGCTGGAGTCCAGGCCA 1007 	RESULT 9 US-09-817-198A-28 US-09-817-198A Sequence 28, Application US/09817198A Sequence 28, Application US/09817198A Sequence 28, Application US/09817198A Patent No. US2020146758A1 Sequence 10. US2020146758A1 Patent No. US2020146758A1 APPLICANT: Will All All All All All All All All All	
Db 1058 TITCICCGIGCATCGIGCTTTCTCTCTCTCCCCCCCCTTCTTTCTCT 1117 Qy 1082 GACCCTCCGGIGCGTTTCGIAICAAGCTCCTCAAACCCCGGIGTGTC 1141	Db 1118 GACCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAAACCCCGTCCCCGTGTGTC 1177	Oy 1142 CTGCTGTGTGCGCTCTTTCCTTCCTA 1176	RESULT 8 US-10-363-616-74 ; Sequence 74, Application US/10363616 ; Publication No. US20040044181A1	0	CURRENT APPLICATION NUMBER: US/10/363,616 CURRENT FILING DATE: 2003-03-03 PRIOR APPLICATION NUMBER: 09/654,935 FRIOR FILING DATE: 2000-09-01	NUMBER OF SEQ 1D NOS: 450 SEQ 1D NO 74 EBNGTH: 1054 TYPE: DNA TYPE:) OKCATURE: FEATURE: NAME/KEY: CDS LOCATION: (81)(719)	<pre>// FEATURE: // NAME/KEY: misc_feature // LOCATION: (1)(1054) // OTHER INFORMATION: n = a,t,c or g US-10-363-616-74</pre>	Ouery Match Best Local Similarity 99.6%; Pred. No. 1.86-265; Best Local Similarity 99.6%; Pred. No. 1.86-265; Matches 1002; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Qy 2 GCCCGCTGCCCCCCCCCCCCCCTCCCCCCCCCCCCCC	

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100.0%; Pred. No. 1.9e-146;
tive 0; Mismatches 0;
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                                                                                    1316 TGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGAAAC 1375
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Patent No. US20020146758A1
GENERAL INFORMATION:
TITLE OF INVENTION: INCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT ELLING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 601
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                                                                                                                                                                            1376 AGCAACCGGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCAGAG
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Pred. No. 1e-154;
1; Mismatches 1; Indels
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Best Local Similarity 99.7'
Matches 599, Conservative
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ORGANISM: Homo sapien
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US-09-817-198A-29
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                                                                                               3042 CIGCACCIGCIGITIGAGACICCATCCAGCCCCAGGCACGCCACCIGCICCIGAGCCIC
                                                                                                                                                                                                                         3102 CACTATCTCCCTGTGACGGGTGAACTTCGTGTACTGTGTCTCGGGTCCATATATGAATTG
2922 AAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGG
                                                                      2982 CATGICITGAGGCCCAGACIGITAAGCAGGCICIGCIGGCCCIGITTACICGICACCACCI
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 597
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. Sequence 507, Application US/09764868

. Patent No. US20020168711A1

; GENERAL INFORMATION:
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MAME/KEY: SITE
LOCATION: (484)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (538)
OTHER INFORMATION: n equals a,t,g,
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; OTHER INFORMATION: n equals a,t,g,
US-09-764-868-507
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ORGANISM: Homo sapiens
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Sequence 30, Application US/09817198A

Patent No. US20020146758A1

GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REPREMENCE: CLOOL1188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT PILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PSESSEQ for Windows Version 4.0

LENGTH: 601
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                       146 CCGAGGCCCAGCGAACTCTTCGAAAACCTGGTGCTGGTGCTGAGTCCTGTGTGGGGCCCC
                                                                          ACACGACACCCCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGGCTTTGCC
                                                                                                   ACACGACACCCCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGCTTTGCC
                                                                                                                                                    CTGCTGCTGTCTCGTGTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCCTGC
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ORGANISM: Homo sapien
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Best Local Similarity
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                                   TCCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCCATATCTCCCTGTGAGGGGTGAAC 420
                                                                                                                            Tredigiacrereredegrecararargaarreregecaegerrearerarraaac 480
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APPLICANT: Magher, Madeleine Joy
APPLICANT: Xing, Gordon E.

APPLICANT: Magher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001.07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 481;
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14.7%; Score 477.4; DB 9;
Best Local Similarity 99.4%; Pred. No. 3.6e-121;
Matches 478; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                      Sequence 303, Application US/09920300A Patent No. US20020136728A1 GENERAL INFORMATION:
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LOCATION: 417, 461

OTHER INFORMATION: n = A,T,C or G

US-09-920-300A-303
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ORGANISM: Homo sapiens
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Patent No. US20020146758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REFERENCE: CL001188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ.ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.8
Matches 516; Conservative
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; ORGANISM: Homo sapien
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GenCore version 5. Copyright (c) 1993 - 2004 Co OM nucleic - nucleic search, using sw model Run on: March 21, 2004, 04:56:29 ; Sear	Title: US-09-817-198C-1 Perfect score: 3257 Sequence: 1 tgcccgctgcccgccgcag Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 27513289 seqs, 14931090276 resi	Total number of hits satisfying chosen parameters Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Listing first 45 summaries	H	12: gb_est3:* 13: gb_est4:* 14: gb_est5:* 15: em_estfun:* 16: em_estom:*	17; em gss inv:* 18: em gss inv:* 20: em gss inv:* 21: em gss inv:* 22: em gss mus:* 23: em gss mus:* 24: em gss nus:* 25: em gss nus:* 26: em gss rod:* 27: em gss rod:* 26: em gss rod:* 26: em gss rod:* 27: em gss rod:* 26: em gss rod:*	: gp

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1837 GAAGAGCATTTCCTCAGACTCCCAGGCGGAGGACTGAGCCTAGCCTTCAGCAAGGT 1896		CCTCCAAAAGAAGAAGAAGAACATCATCATCTTCCTCCTGACTTACCAAACCAGG AAAACAGCAGGAAGAGGCTCAGGACTTAGGGACAGGTATAGCTTAGATGAGAAA	2677 CTTCACCAGGGACTTGAGAGTTATATTGGCAGTGGCTCCAATCTGTGGACCAGTATT 2736 [

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| organism="Homo sapiens" |
| mol type="mrNype" mrNype" mrNyp
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윰	661	GCTCGTGGGGAAGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCCTCGTGGGTG 720
දු පු	1261	GGCCAAAGGCTACAGGGGGCTTCTTCCTCTTCCCCCACTGTCCCTCATGTGCCA 1320
À i	1321	TGGGCCTGCCTCCCCAGTGACCTGCGAAGTGGAGCATCGAGGTAGGAGGGAAACAGCAA 1380
o do i	1381	381 CCGGGGAGTCCTCGAGGCTGCCCTACCTCTACCTTTCCCCGACCAGAGCTTTG 1440
g &	841 1441	CCGGGGGGGCTCCTCGGGGCCTCCTCTTTGGGGAACTGACCAACGCAGGGGTTCAGGCTTCAGGTAGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGTAGCTTCAGGTTCAGGCTTCAGGTTCAGGCTTCAGGTTTCAGGTTCAGGTTCAGGTTCAGGTTTCAGGTT
qa	901	CCTTGCTTGGCTGCCCGCCTGCTTTGGGGAACTGAGCTCAGAGGCAGGTGCTTCAG 960
λo	1501	
Db	961	AGAAGGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCTACCTCCCA 1020
දු දු	1561	TGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCAAGGC 1620
à	1621	CTGTGGGTACTCCAGGGGAAGGAGCCCTGGGGTCAGTGACACTGTCAGGCCAACCAT 1680:
qq	1081	CTGTGGGTACTCCAGGGCAAGGGGCCCTGGGGTCAGTGACACTGTCAGGCCAACCAT 1140
ογ.	1681	GCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGA 1740
ag	1141	GCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTATGA
ò i	1741	GCAAGGGAGAGCTGGCCAGGGACAGCAGTTTGCACAGGGGGAATGTAGCAACAGGC 1800
අ	1201	GCAAGGGAGGAGCTGGCCAGGGACAGCAGTTTGCACAGAGGGAGG
è e	1801	GGGCCTCCTAGGCCCCATCTTCCTTAGGTAAGAAGACATTTCCTCAGACTCCCA
'n	1861	GGCGGAGGACTGAGCCTTCAGCAACCAAGGTTCTCCTGGGACCCCAAAGTTTATGG 1920
qq	1321	GGCGGAGGACTCAGCCTTCAGCAACCAAGGTTCTCCTGGGACCCAAGTTTATGG 1380
ò	1921	GAGAAGGCAAAGACTTCATGGGAAGAAGAAAGGCCCTGGGTAGAAACGCTTGGTG 1980
Д	1381	GAGAAGGGCAAAGACTTCATGGGAAGAGAAGGAAGGAAGG
ζŏ	1981	CIGITCICITICGCCTITAAGACAGAAGGCCTCATCTIGCCCTCTACCTCCTGATAGGCTT 2040
DP DP	1441	CIGITCICITIGGCCITIAAGACAAAGCGCTCATCTIGCCCTCTACCTCCTGATAGGCTT 1500
λ	2041	GAGGGTTTGCCAACCACACTGTGGCTACAGGTGGAGGGAAGAGGACTCCTTCCT
Dp Dp	1501	GAGGGTTTGCCAACCACACTGTGGCTACAGGTGGAGGGAAGAGGACTCCTTCCT
λΌ	2101	TGCTATGTTCAGGAAGTTTCTTTAACCCCATATGGCCCAAGAGTAGCTCGTAGGAGGCCC 2160
Q	1561	TGCTATGTTCAGGAAGTTTCTTTAACCCCATATGGCCCAAGAGTAGCTTGTAGGAGGACGCCC
ò	2161	TITAAAGACGGAACAAGTAAITIACCAGTICTACTGGGGTICCTGCCCACGTCCCAAGG 2220
qq	1621	
ò	2221	TGGGCGAGGCCTAGGAAGAGGTCATTCTTAAGCCACACATTAGCTGCACTGCGTGGCTG 2280
qq	1681	
à	2281	
ch Ch	1741	CAGCCAAAACAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAACCAAAATCCAGGGCA 1800

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/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"

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CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
           1 (bases 1 to 1081)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                          GGACTTAGGGACAGGGTATAGCTTAGATGGTGGAAAGCAAAGGAGGAGGAGGAAGTTGTAA 1980
                                                                          ACCATCAAACCTTTCCTCCTGACTTACCAAACCAGAAAACAGCAGGAGAGGGGGCTCA
                                                                                                                                                                                                                    ATCACTGGCTAATGAGAAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGACTGAGGCTGG
                                                                                                                                                                                                                                                                                GCTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGACTTGAGAAGTT
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/uzer=TWAGE:1979433"
/tissue_type="astrocytoma grade IV, cell line"
/lab hose="BLHOB (phage-resistant)"
/clone lib="NLH Grage-resistant)"
/clone lib="NLH GC 98"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: ECRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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AGENCOURT 6575472 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5479433 BM551913

Homo sapiens (human) Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

BM551913.1 GI:18789340

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cgi-bin/cluster.cgi?seq=CSODIO28AG06_DI1486_2&cluster=7307.r.
contact: Feng Liang Email: fliang@Tifetech.com URL:
http://fulllength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO28AG06_DI1486_2.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7307.r
more information about this cluster, see
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 956)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
Unpublished (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI028YM11"
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/tissue type="PlACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not!-oligo (dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2496 AGCAAAGGAGGAGGAAGTTGTAAATCACTGGCTAATGAGAAAAGGAGACAGCTA 2551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 G-AAACAGCAGGAGAGGGTGGCTCAGGACTTAGGGACAGGGTATAGCTTANATGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACTAAGAACCAAAATCCAGGGCACTCATATGTGAAGGATAAGAACCTCACTTAC
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                                                                                                                                                                                                                                                                                            61 TCAGTGACACTGTCAGGCCAACCATGCACTCCACAAAGGGGAGCATTTGGAAATGAAGG
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                                                                                                                                                                             Score 883.4; DB 13; Length 956;
Pred. No. 4e-123;
; Mismatches 9; Indels 5;
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1673

1733

420

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us-09-817-198c-1.rst

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BX397020

915 bp mRNA linear EST 13-MAY-2003
BX397020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI028YM11 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   ACTCCCAGGCGGAGGACTGAGCCTTCAGCAACCAAGGTTCTCCTGGGACCCAAAG 1913
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1 (bases 1 to 915)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                         301 CCAAGGCCTGTGGGTACTCCAGGGCAAGGAGCCCTGGGGTCAGTGACGTGTCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                               541 ACTCCCAGGCGGAGGACTGAGCCTTAGCCTTCAGCAACCAAGGTTCTCCCTGGGACCCAAAG
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                                                                                                                         CAACCATGCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAG
                                                                                                                                                                                                                        GTTAAGAGCAAGGGAGAGCTGGCCAGGGACAGCAGTTTGCACAGAGGGGGAATGTAGC
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Genescope - Centre National de Sequencage
Genescope - Centre National de Sequencage
BP 191 91006 EVRY
Genescope - Centre
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7307.rr
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi1seq=cS0D1028AG06_D11486_L&cluster=7307.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 40"
/note="Grgan: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; coNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                         PGENCOURT 10018726 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:64821955', MRNA Sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2664 row; m column: 12
High quality sequence stop: 555.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Stratagene) and Superscript II R'
Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6482195"
                                                                                                                                                                                                                                             BQ937298.1 GI:22352681
                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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                                | 1. 915 |
| / organism="Homo sapiens" |
| / organism="Homo sapiens" |
| / mol_type="mRNA" |
| / db_xref="taxon:9606" |
| / dlone="CSONIO28YM1" |
| / tissue_type="PlACENTA COT 25-NORMALIZED" |
| / clone_lib="Homo sapiens PlACENTA COT 25-NORMALIZED" |
| / clone_lib="Homo sapiens PlACENTA COT 25-NORMALIZED" |
| / orde="list strand cDNA was primed with a NotI-oligo(dT) |
| / orde="list strand cDNA was primed with a NotI and cloned into the Not I and EcoR V |
| sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                 Gaps
Avenue Genoscope sequence ID : CS0DI028AG06_DI1486_1. Location/Qualifiers
                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                              26.0%; Score 847.2; DB 13; Length 915; 98.3%; Pred. No. 1.1e-117;
                                                                                                                                                                                                                                                                                 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                Best Local Similarity 98.3
Matches 882; Conservative
     Faraday
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/tissue_type="sympathetic trunk"
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/clone lib="tupski sympathetic trunk"
/clone lib="tupski sympathetic trunk"
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/note="vector: pcMV-SPORT6 (Life Technologies); Site_1:
Not!; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
S-'cGACCAGCGCGCGCGCGCGCGCGCCT(15)-3'. Size selected
S-'GACTAGTTCTAGATCGCAGCGCCGCCCT(15)-3'. Size selected
: Lkb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
Technologies." BGV16774 908 bp mRNA linear EST 16-JUL-2002 AGENCOURT 8217893 Lupski_sympathetic_trunk Homo sapiens CDNA clone IMAGE:6187941 5', mRNA sequence. ä CITICICIGACCCCICCCCICCGGIGCGITICGIAICAAAGCICCTCAAACCCCGICCCC 1133 CGTGTGTCCTGCTGTGCAGCTCGCTCTTCCTTCCTAAGCTATCCAAGGGATG 1193 CGTGTGTCCTGCTGTGTGCACCTCGCTCTTTCCTTCCTTACCTATCCAAGGGGATG 180 801 GAAAGAACCATCAAACCTTTTCTNCTGACTTACCAAACCAGG-AAACAGCNAGAGAGGGT 859 9 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 908)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999) Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13582 row: 1 column: 22 GCTGCTCCTTTCTCCCGTGCATCGTGTCTCTTCTCTGCTTTTTTCTCTCTTCCCCCCACTTCT 860 GGCTCAGGACTTAGGGACAGGTATAGCTNANATGGT-GAAAGCAAAGGAGAGCAGG 2455 GCCTCAGGACTTAGGGACAGGCTATAGCTTAGATGGTGGAAAGCAAAGGAGGAGGAGG 3; Length 908; Indels 25.8%; Score 840.2; DB 13; ilarity 97.6%; Pred. No. 1.3e-116; Conservative 0; Mismatches 19; 1 High quality sequence stop: 638.
Location/Qualifiers
1. 908
/organism="Homo sapiens"
/mol rype="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:6187941"

us-09-817-198c-1.rst

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                                                                                                                                                                                                                                                                                    /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7307.r For more information about this cluster, see http://www.genoscope.rms.fr/
cgi-bin/cluster.cgi?seq=CSOBAA015ZB10 CS01419_1&cluster=7307.r.
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOBAA015ZB10_CS01419_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.7%; Score 837.8; DB 13;
ilarity 97.9%; Pred. No. 2.9e-116;
Conservative 0; Mismatches 18;
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/clone="CS0D1028YM11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 848; Conserv
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Genoscope - Centre National de Sequencage
BP 191 91006 EYRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 929)
S. Li,W.B. Gruber,C., Jessee,J. and Polayes,D.
Full.length cDNA libraries and normalization
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7307.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAF024ZB10_AF02283_2&cluster=7307.r.
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BX348287.1 GI:30369275
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BQ220195.1 GI:20401595 EST.
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                                          CGTTTCGTATCAAAGCTCCTCAAACCCCGTCCCCGTGTGTCCTGCTGTGTGCAGCTCGC 1159
                                                                                                                                          1160 TCTTCCTTCCTTCCTAAGCTATCCAAGGGATGGACCCAGGCTCGTGGGGAGGTTCCAC 1219
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1 (bases 1 to 901)

11 HymGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMl331 row: e column: 07
High quality sequence stop: 606.
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Best Local Similarity 98.73
Matches 838; Conservative
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Best Local S:
Matches 868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/mol_type="mRNA"
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/clone="CSODIOSYM11"
/tissus_type="Flacenta COT 25-NORMALIZED"
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EOOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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               http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAF024ZB10_AF02283_2
Location/Qualifiers
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                                                                                                                                                                                                                                                                                 Score 807.8; DB 13; Length 929;
Pred. No. 9.2e-112;
0; Mismatches 26; Indels 8;
Contact : Feng Liang Email : fliang@lifetech.com URL
                                                                                                                                                                                                                                                                                  24.8%;
96.4%;
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Matches 899; Conservative
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/dlone="IMAGE:5015713"
/tissue type="small cell carcinoma"
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/clone lib="NHH MGC_7"
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                                                                                               1266
                                                                                                                                                                                                                                                                                                                                                                                                                                           BI118034 924 bp mRNA linear EST 26-JUN-2001 602867301F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:5015713 5', mRNA sequence.
BI118034
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DcTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCMR825 row: b column: 02

High quality sequence stop: 893.

Location/Qualifiers
GTGTGCAGCTCGCTCTTTC--1TCCTTCCAAGCTATCCAAGGGGATGGACCCAGGCTCGG
                                                                                               GGGGAGGGTTCACCTTGGGATCCGGGAAGAACCCTCC-CCCTGCCTTGGGGGGGGGCCAA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 7.8e-111;
0; Mismatches 54; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="teratocarcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/clone lib="NIH MGC 1109"
/note="Organ: ovary, Vector: pOTB7; Site_1: EcoRI; Site_2:
Xho1; cDNA made by oligo-dT priming. Directionally cloned
inco EcoRI/Xho1 sites using the following 5 adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Burkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library.
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         CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
http://image.lln.gov
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                                                                                                                                                                                                                   1. .1046
/organism="Homo sapiens"
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/db xref="taxon:9606"
/clone="IMAGE:5804597"
Fissue Procurement: ATCC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1046)

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AUTHORS
TITLE
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/Lisbure_type="teratocarcinoma, cell line"
/clone_lib="NIH#018 (phage-resistant)"
/clone_lib="NIH#02 (109"
/note="Organ: Ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhoI sites using the following S' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                             2266
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                                                                                                         2267 GCACTGCGTGGCTGCCGAAAACAAAGGAACTGGGTGTTGAGTATTCATCAACTAAGAAC 2326
                                                                                                                                                                    2327 CAAAATCCAGGGCACTCATATGT-GAAGGATAAGAACC--TCACTTCCTTACTCCTCCAA 2383
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
frow: f column: 22
High quality sequence start: 32
High quality sequence etop: 727.
Location/Qualifiers
CCACCGTCCCAAGGTGGGCGAGGCCTATGAAGAGGGTCATTCTTAAGCCACACACTTAGCT
                                                                                                                         CCACCGTCCCAAGGTGGGCGAGGCCTAGGAAGAGGGTCATTCTTAAGCCACACATTAGCT
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                                                                                                                                                                                                                                2384 AAAGAAGTGGGG-AAAGAACCATCAAACCTTTCC 2416
                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6585046"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT 10440477 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:5598564 5', mRNA sequence.
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Bukaryotti.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 820)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
  97
                                                                               98 AGCAAAGGAGAGGAGGAAGTTGTAAATCACTGGCTAATGAGAAAAGGAGACAGCTAACTC
                                                                                                                                                                                  638 CCACCTCTGCACCTGCTGTCTTGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCCTG
38 GGAAACAGCAGGAGGGGTGGCTCAGGACTTAGGGACAGGGTATAGCTTAGATGGTGGAA
                                                                                                                                                       TAGGATGAAGCTGTGACTAGGCTGGAGTTGCTTCCTTGAAGATGGGACTCCTTGGGTATC
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/note=_organ: ovary; Vector: pOTB7; Site_1: EcoR1; Site_2: Xhol; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xhol sites using the following S' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superseript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                             661 GAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTGTGTCTCGGGTCCATATA 720
                                                                                                                                                                                                                             721 TGAATTGTGAGGAGGGTTCATCTATTTTAAACACAGATGTTTACAAAATAAAGATTATT 780
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 863)
                          601 ACCACCTCTGCACCTGCTGTCTTGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCCT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can t
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2796 row: i column: 19
High quality sequence stop: 679.
Location/Qualifiers
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AGENCOURT 10253405 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6585115 5', mRNA sequence.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="texon:9606"
/clone="IMAGE:6585115"
/lssue_type="textatocarcinoma, cell line"
/lab host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_109"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                  3215 CAAACCACCAAAAAAAAAAAAAA 3239
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Tissue Procurement: ATCC
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/db xref="taxon:966"
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/tissue type="teratoarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 109"
/note="Organ: ovary; vector: pOTB7; Site_1: EcoR1; Site_2: Note="Organ: ovary; vector: pOTB7; Site_libectionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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                    CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2831 row: j column: 04
High quality sequence stop: 668.
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                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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Search completed: March 21, 2004, 11:01:47 Job time : 7335 secs

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GenCore version 5.1.6
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March 15, 2004, 11:08:42; Search time 60 Seconds (without alignments) 998.335 Million cell updates/sec Run on:

US-09-817-198C-2

score: Title: Perfect

1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC 212 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

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geneseqp2003as:* geneseqp2003bs:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abp62882 Human pol	Aae29096 Human Ras	Aau17136 Novel sig	Adb93844 Human nov	Aab41604 Human ORF		Aaul7555 Novel sig	Adb94263 Human nov	Abb70670 Drosophil	Ade58121 Human Pro	و	Abp41333 Human ova	6	Ade58125 Human Pro	Aab58196 Lung canc	Aab09979 Human Rab	Aab19165 Amino aci	Aab95340 Human pro	Aab56993 Human pro	Abg07266 Novel hum	Abb71647 Drosophil	Aag67154 Amino aci	Aab92628 Human pro	Abp65204 Hypoxia-r	Aab09982 Canine Ra
ID	ABP62882	AAE29096	AAU17136	ADB93844	AAB41604	ADE58127	AAU17555	ADB94263	ABB70670	ADE58121	ABB11916	ABP41333	ADE83429	ADE58125	AAB58196	AAB09979	AAB19165	AAB95340	AAB56993	ABG07266	ABB71647	AAG67154	AAB92628	ABP65204	AAB09982
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## ALIGNMENTS

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antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                      Human; vulnerary; dermatological; neuroprotective; nootropic; cancer;
                ABP62882 standard; protein; 212 AA
                                                                    Human polypeptide SEQ ID NO 319.
                                                  (first entry)
                                                  14-OCT-2002
                                  ABP62882;
RESULT 1
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Homo sapiens.

WO200218424-A2.

07-MAR-2002.

31-AUG-2001; 2001WO-US027093.

01-SEP-2000; 2000US-00654935

(HYSE-) HYSEQ INC.

Wang J; Zhang J, Ren F, Zhar Wehrman T; Zhou P, Xue AJ, u C, Drmanac RT, Asundi V, Znov Tang YT, Zhao QA,

WPI; 2002-583321/62.

N-PSDB; ABQ93361.

New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzhaher's Parkinson's, Huntington's, amylotrophic lateral solerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.

Claim 20; SEQ ID NO 319; 284pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (I), (II) and (III) are useful for diagnostic evaluation of disorders (I) is useful for gene therapy of diseases and (II) can be used for

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therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Albahmer's, Parkinson's by Huntington's and maylotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained to. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Ras-like protein; inflammation; cell proliferation; apoptosis; immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis; parkinson; disease; metring disease; carchexia; mycardial infarction; osteoporosis; atherosclerosis; glomerulonephritis; Crohn's disease; irritable bowel syndrome; multiple sclerosis; osteoarthritis; allergy; pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic; Sjogren's syndrome; infection; transgenic; gene therapy; nootropic; gout, neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic; ophthalmological; tranquilliser; cancer; stroke; Grave's disease; AIDS;
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:e= "Casein kinase II phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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                                                                                                                                                                                Length 212;
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i36. .141
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note= "ATP/GTP binding site motif A"
                                                                                                                                                                              100.0%; Score 1105; DB 5;
100.0%; Pred. No. 1.4e-108;
tive 0; Mismatches 0;
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/note= "N-glycosylation site"
206. .208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE29096 standard; protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma; anaemia; drug screening
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                               Local Similarity
les 212; Conserv
                                                                                                                                                   Sequence 212 AA;
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Matches
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The invention relates to human Ras-like protein and its corresponding nucleic acid. The Ras-like protein and DNA is useful in the development of nucleic acid. The Ras-like protein and DNA is useful in the development of human therapeutics and diagnostic compositions. They are useful in the diagnosis, prevention and treatment of inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS and other inflectious or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia, ischaemic injuries e.g. myocardial infarction, stroke or repertusion injury, toxin-induced diseases such as alcohol-induced liver damage or cirrhosis, osteoporosis or cancer. They are also used to treat disorders associated with inflammation including allergies, atopic dermatitis, atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus, catherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus, catherosclerosis, strumm, or viral, bacterial, fungal, parasitic, proteozeal or haminthic infections. The antibodies of the invention are useful in the pharmacognomic analysis or for tissue typing. The transgenic animals are useful for studying the function of a Ras-like protein is used in drug screening assays and its activity. Ras-like protein is used in cargenic an human Ras-like protein is used in gene therapy. The present
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/note= "Protein kinase C phosphorylation site"
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Best Local Similarity 100.0%; Pred. No. 1.4e-108;
Matches 212; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                     Beasley EM;
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                                                                                                                                                                                                                                                   Gan W, Ye J, Di Francesco V,
                                                                                                                            27-MAR-2002; 2002WO-US009328
                                                                                                                                                                     27-MAR-2001; 2001US-00817198
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AAU17136 standard; protein; 401 AA

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2000US-0232401P.
2000US-0233063P.
2000US-0233064P.
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2000US-0234274P.
2000US-0234997P.
2000US-0234998P.
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                                                         08-SEP-2000;
14-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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20-OCT-2000;
20-OC
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17-NOV-2000;
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                                                                                                                                                 Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; anti-ifflammatory; anti-ifflammatory; anti-ifflammatory; anti-ifflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; organ transplant rejection; infection; hepatitis C; blood disorder; organ transplant rejection; and isorderical cancer; disorder; disorder; disease; neurodegenerative disorder; Alzheimer's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovesscular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; acquired immune deficiency syndrome.
                                                                                                       Novel signal transduction pathway protein, Seq ID 701
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2000US-021647P

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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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28-JUN-2000
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Homo sapiens.
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                                                              ADB93844;
                                                            the invention traders to mover according to the antibody to (I) are useful for diagnosting, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune clasorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital arbitration), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin annormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders primary haematopoietic disorders, hyperproliferative disorders (e.g. ducher's disease and cancer), neurodegentrative disorders (e.g. Alzheimer's disease and cancer), neurodegentrative disorders (e.g. Alzheimer's disease Parkinson's (e.g. stroke), renal disorders (e.g. Glomerulonephritis), cardiovascular disorders (e.g. arthythmia), respiratory disorders, cardiovascular disorders (e.g. Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of disease), reproductive system disorders (cirrhosis), as stimulators of higher affinity antibodies, and as a means to induce (unour proliferation to higher thouse servine deficiency syndrome (ADDS). AAU17059-AAU17683 represent novel signal transduction pathway protein, amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel isolated polypeptides (I), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 RMRASNELALAELEEEEGKPEGPANSSKTCWC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 1; SEQ ID NO 701; 880pp; English.
                                                                                                                                                                                                                                                                                                 Ruben SM;
                                                                                    2000US-0256719P.
2000US-0251479P.
2000US-0251856P.
                                                 2000US-0251030P.
2000US-0251988P.
                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                2000US-0250160P
                                  2000US-0250391P
                                                                                                                                     2000US-0251868P
2000US-0251869P
                                                                                                                                                                                         2000US-0251990P
                                                                                                                                                                                                             2000US-0254097P
                                                                                                                                                                                                                           05-JAN-2001; 2001US-0259678P
2000US-0249300P
                                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                    WPI; 2001-465460/50.
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS27053.
                                                                                                                                                                                         08-DEC-2000;
                                                 05-DEC-2000;
                                                                                    05-DEC-2000;
06-DEC-2000;
                                                                                                                                     08-DEC-2000;
                                                                                                                                                           38-DEC-2000;
                                    01-DEC-2000;
                  01-DEC-2000
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human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; immunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction;
                                                                                                                                                                                                                                                                                                                                                                    increased serum immunoglobulin concentration
                        ADB93844 standard; protein; 401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001; 2001US-00764868
                                                                                                                                       04-DEC-2003 (first entry)
                                                                                                                                                                                              Human novel protein #78.
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05-SEP-2000;
08-SEP-2000;
ADB93844
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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the perturbed by the presence or amount of expression of the polypeptide. Which involves contacting the polypeptide is also useful for identifying a binding partner and determining whether the binding partner ceffects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid a medical condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or basence of a mutation. The polypeptide, the nucleic acid and an antibody to the polypeptide are useful acid and an antibody are useful as immunosuppressive agents, the nucleic acid and the antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. The protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format direct from the protein uspic organ/sequence. The sequence chimined in electronic format direct from the protein and an antipod or this patent did not form part of the protein.
                                                                                                                                                                                                                                                                                                                           New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 701; 345pp; English
                                                                                                                                                                                                    Barash SC;
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
                                                                                                                                                                                                 Rosen CA, Ruben SM,
                                                                                               ROSEN C A.
RUBEN S M.
BARASH S C.
                                                                                                                                                                                                                                                  WPI; 2003-719985/68
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                                                                                                    ROSE/)
                                                                                                                         (RUBE/)
(BARA/)
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Sequence 401 AA;

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146
                                                                                                                        61 IWDTAGQERYQTITKQYYRRAQGIFLUYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                   121 NKADBEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                 206
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                                                                              27 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                           1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                              Gaps
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100.0%; Score 1105; DB 7; Length 401; 100.0%; Pred. No. 3.5e-108;
                              0; Indels
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                              0; Mismatches
            Best Local Similarity 100.
Matches 212; Conservative
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Query Match
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RMRASNELALAELEEEEGKPEGPANSSKTCWC 238

207

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RESULT 5 AAB41604

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AAB41604 standard; protein; 218 AA.
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(first entry) 38-FEB-2001

Human ORFX ORF1368 polypeptide sequence SEQ ID NO:2736.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
W immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
W hypotensive; dermatological; immunosuppressive; antiinflammatory;
W antiviral; antibacterial; antifungal; antirheumatic; antiinkroid;
antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
w neurodegenerative disorder; osteoarthritis; graft vs host disease;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
W cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
Cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
bone damage; cartilage damage; antiinflammatory disease; coagulation;
w thrombosis; contraceptive.

Homo sapiens

WO200058473-A2.

15-0CT-2000

31-MAR-2000; 2000WO-US008621.

02-APR-1999; 99US-0127636P. 05-APR-1999; 99US-0127728P. 30-MAR-2000; 2000US-00540763. 99US-0127607P 11-MAR-1999;

(CURA-) CURAGEN CORP.

Leach M; Shimkets RA,

WPI; 2000-602362/57. N-PSDB; AAC75813. Novel nucleic acids and peptides derived from open reading frame X, disorders, useful for treating e.g. cancers, proliferative disorde neurodegenerative disorders and cardiovascular disease.

Claim 11; Page 1979-1980; 5507pp; English.

which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiporiatic; antimarkintic; immunosuppressant; immunostimulant; cardiant; thrombolyvic; canduant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressate; antiinflammatory; antibacterial; antiviral; antifrumatic; antiinflammatory; antibacterial; antiviral; antifrumgal; antirhenwatic; antithyroid; antibacterial; antiviral; antifrumgal; antirhenwatic; antithyroid; antibacterial; co, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative used to treat cancers, proliferative disorders, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cablesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive

Sequence 218 AA;

Query Match

98.8%; Score 1092; DB 3; Length 218;

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AAU17555;
                                                                                                                                                                                               Query Match
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               ij
                                                                                          61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                61 IMDTAGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                               174
                                                                                                                                                                        121 NKADEEQKRQVGREQGQQKCPSLQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                              Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                        60
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                                                        1 MAKQYDVLPRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRLQ
                                        1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                               121 NKADEEOKROVGREOGO-----OLAKEYGMDFYETSACTNINIKESFTRLTELVLOAHR
               Gaps
               9
               Indels
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 Pred. No. 3.4e-107;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2002; 2002WO-US025765
 97.2%;
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(FARB ) BAYER AG.
                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-268312/26.
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENBANK; AAA41995
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                   Matches 212;
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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antinflammatory; anti-HIV; antibacterial; antinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; isochaemis; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1077; DB 7;
Pred. No. 1.3e-105;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 RMRASNELALAELEEEGKPEGPANSSKTCWC 212
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24-FEB-2000; 2000US-0184664F.
02-MAR-2000; 2000US-01863F.
16-MAR-2000; 2000US-0189874F.
17-MAR-2000; 2000US-0190076F.
18-APR-2000; 2000US-019123F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 97.6 Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 212 AA;
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2000US-0214886E

2000US-0216880E

2000US-0216880E

2000US-0217487E

2000US-0218290E

2000US-022856E

2000US-02386E

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2000US-0240960P.
2000US-0241221P.
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08-SEP-2000; 2
08-SEP-2000; 2
08-SEP-2000; 2
08-SEP-2000; 2
12-SEP-2000; 3
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14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
          28 JUN - 2000)
30 JUN - 2000)
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11 JUL - 2000)
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20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241826P.
01-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0249201P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024928P.
05-DEC-2000; 2000US-025186P.
06-DEC-2000; 200US-025186P.
06-DEC-2000; 200US-025186P.
06 (HUMA-) HUMAN GENOME SCI INC 05-JAN-2001; 

Ruben SM; Rosen CA, Barash SC, WPI; 2001-465460/50 N-PSDB; AAS27472. Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

Claim 1; SEQ ID NO 1120; 880pp; English.

The invention relates to novel isolated polypeptides (I), and polymuclectides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

2000US-0225268P. 2000US-0225270P. 2000US-0225447P.

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transplant rejections and graft versus host disease, infectious diseases
transplant rejections and graft versus host disease, infectious diseases
cc (e.g. hepatities C), bleeding disorders, haemoglobin abnormalities and
cother blood-related disorders (sickle cell anaemia), myeloproliferative
disorders, primary haematopoietic disorders, hyperproliferative disorders
cd saucher's disease, parkinson's disease, chromosomal abnormalities
cc Alzheimer's disease, parkinson's disease, chromosomal abnormalities
cc Alzheimer's disease, parkinson's disease, chromosomal abnormalities
cc Alzheimer's disease, parkinson, edicorders (e.g. arrhythmia),
cglomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
cspithelial cell proliferation, endocrine disorders (e.g. Addison's
disease), reproductive system disorders, gastrointestinal disorder
clinflammatory disorders), liver disorders (cirrhosis), as stimulators of
B-cell responsiveness to pathogens, activators of trichls, to induce
clinpathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
AAU17050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences of the invention
               $8666666666666666666688
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61 IMDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                              84 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQXILIG 143
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                                                                                                        1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                        24 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                        0; Gaps
Ouery Match 75.3%; Score 832; DB 4; Length 188; Best Local Similarity 97.6%; Pred. No. 1.1e-79; Matches 160; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                   NKADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTR 164
                                                                                                                                                                                                                                                                                                                                                                   144 NKADEEQXROVGREQGOXLAXEYGMDPYETSACTNLNIKESFTR 187
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## ADB94263 standard; protein; 188 AA ADB94263; RESULT 8 ADB94263

04-DEC-2003 (first entry) Human novel protein #497.

human, autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; minunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration.

Homo sapiens

US2002168711-A1

14-NOV-2002

17-JAN-2001; 2001US-00764868 31-JAN-2000;

2000US-0216880P. 2000US-0217487P. 2000US-0217496P. 2000US-0218290P. 2000US-0180628P. 2000US-0214886P. 2000US-0216647P. 2000US-0224518P 2000US-0224519P 11-JUL-2000; 04-FEB-2000; 28-JUN-2000; 07-JUL-2000; 14-AUG-2000; 14-AUG-2000;

14-AUG-2000; 2000US-0225757P.
14-AUG-2000; 2000US-0225757P.
13-AUG-2000; 2000US-0225758P.
22-AUG-2000; 2000US-0228924P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229343P.
21-SEP-2000; 2000US-0239342P.
21-SEP-2000; 2000US-0239379P.
22-SEP-2000; 2000US-0236369P.
23-SEP-2000; 2000US-0236369P.
23-SEP-2000; 2000US-0236369P.
23-SEP-2000; 2000US-0236369P.
23-SEP-2000; 2000US-0236369P.
23-SEP-2000; 2000US-0236369P.
23-CCT-2000; 2000US-0236369P.
02-CCT-2000; 2000US-0237039P.
02-CCT-2000; 2000US-0237039P.
02-CCT-2000; 2000US-0237039P.
02-CCT-2000; 2000US-0237039P.
02-CCT-2000; 2000US-0237039P.
02-CCT-2000; 2000US-0237038P.
2000US-0251869P 01-NOV-2000; 17-NOV-2000; 08-DEC-2000; 

(ROSE/) ROSEN C A. (RUBE/) RUBEN S M. (BARA/) BARASH S C.

Barash SC Rosen CA, Ruben SM,

WPI; 2003-719985/68 N-PSDB; ADB93640 New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's disease

Claim 11; SEQ ID NO 1120; 345pp; English

The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide is also useful for identifying a binding partner to the polypeptide, which involves contacting the polypeptide with a binding partner and determining whether the binding partner of effects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition and subject, which involves determining the presence or absence of a mutation in The nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or based on the presence or absence or the presence or absence of the mutation. The polype

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disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide, the nucleic acid and the antibody are useful as immunosupressive agents as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. Present sequence represents the amino acid sequence of a novel human protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at seqdata.uspto.gov/sequence.html?DocID=20020168711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental blology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLiG176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
                                                                                                                                                                                                                                                                                                                                                                                        84 IMDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKMVSDVDEYAPEGVQXILIG 143
                                                                                                                                                                                                                                                                                                                                                                     IMDTAGOERYQTITKQYYRRAQGIFLUYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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genes from Drosophila and for elucidating cell signaling and cell-cell
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autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 38802; 21pp + Sequence Listing; English
                                                                                                                                                                                                                  Score 832; DB 7; Length 188;
Pred. No. 1.1e-79;
); Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 38802.
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 97.6
Matches 160; Conservative
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                                                                                                                                                                                     Sequence 188 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragmen derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent
                                                                                                                                                                       ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                     MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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6
                                                                                          Length 204;
                                                                                                                       50; Indels
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                                                                                         49.5%; Score 546.5; DB 4, 49.8%; Pred. No. 2.3e-49; ive 47; Mismatches 50
                                                                                                                                                                                                                                                                                                                                        180 LEMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                    177 RESAENOERVIIDRRNQEKAP----GYSKCC 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Protein P24407, SEQ ID NO 3992
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26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L4-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                       Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-268312/26
                                                                                                         Best Local Similarity
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                                                              Sequence 204 AA;
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that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the aptivity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides or their antibodies. The polynucleotide or the compound that pain and a pharmaceutical composition comprising a medicament for treating pain and a pharmaceutical composition comprising a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
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Sequence 207 AA;

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120
                                                                                                                                 61 IWDTAGGERFRITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEBHASADVEKMILG 120
                                                                                                                                                                      121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                      9
                                                                          1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
                                  0; Gaps
       49.3%; Score 545; DB 7; Length 207;
                                 43; Indels
                       Pred. No. 3.4e-49
                                  45; Mismatches
                       52.9%;
Query Match
Best Local Similarity 52.9%
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ABB11916 standard; peptide; 213 AA. 11-JAN-2002 (first entry) ABB11916; 

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemicaxis; chemokinesis; brincholysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; lymphoid cell disorder; arthritis; atherosclerosis; coronary heart diseas; arterial isofaemis; bone disorder; osteoporosis; vascular growth disorder; issue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; Human rab8 homologue, SEQ ID NO:2286.

Homo sapiens

antifungal; vulnerary; antiulcer.

cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;

WO200157188-A2

09-AUG-2001.

05-FEB-2001; 2001WO-US003800.

03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875. 

(HYSE-) HYSEQ INC

Tang YT, Liu C, Drmanac RT;

2001-457740/49. N-PSDB; ABA09160 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

Claim 20; Page 276; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10981-ABB12330 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a curleotide of the invention, methods of producing the novel polypeptides of the invention, methods of identifying compounds which polypeptides in a sample, and methods of identifying compounds which polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell inferential interapeutic applications. The polypeptides of the invention may have various activities, stem cell growth factor activity; immunomodulatory activity; tissue growth activity; cell interaction or cell invention activities; activity; tissue growth activity; immunomodulatory activity; activity; tissue growth activity; immunomodulatory activity; activity or inhibin-related activities; chrombotic cr chemokinetic activities; peeper or largand activities; or may be invocanced; or chemokinetic activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliozating medical cancers, haemacopoletic disorders (e.g., mypopetides and nucleotides or cancers, haemacopoletic disorders (e.g., mypopetides and nucleotides or arterial ischaemia, bone disorders (e.g., mypopetides with factors), conditions (e.g., asthma or arthritis), creating ichaemia, bone disorders (e.g., mypopetides with growth, polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promoce wound repair (or nucleic acids encoding them) may be used to promoce wound repair (or nucleic acids encoding them) may be used to promoce wound repair disease or activities and ulcers), when the growth. For example, such polypeptides with growth. For example, such polypeptides with grow

Sequence 213 AA;

ö 0; Gaps 49.3%; Score 545; DB 4; Length 213; 52.9%; Pred. No. 3.6e-49; ive 45; Mismatches 43; Indels Query Match
Best Local Similarity 52.9%

99 1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNBFHSSHISTIGVDFKMKTIEVDGIKVRIQ 

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61 IMDĮAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120

121 NKADEBOKROVGREGGGGLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180  us-09-817-198c-2.rag

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymuciaculars, and the against indian ovarian and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorines, endocrine disorders, infertions (e.g., champadia, HV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and cancer and infertions (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may
                                                                                                                                                                                                                                                                                                                                                      ovarian cancer; breast cancer; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst, dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forenisc analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
127 NKCDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIKAKMDKKLEGN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use
                                                                                                                                                                                                                                                                                                                                          ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                Human ovarian antigen HCGMA67, SEQ ID NO:2465.
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                                                                                                                                                                            ABP41333 standard; protein; 221
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                                                                                                                                                                                                                                                         (first entry)
                                       181 RMRASNE 187
                                                                            187 SPQGSNQ 193
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                                                                                                                                                                                                                                                           23-AUG-2002
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                                                                                                                                                                                                                   ABP41333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment,
further be used for gene therapy, chromosome mapping, in the identification of individuals and in forenate analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                               16 AKTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQI
                                                                                                                                                                                                                                                                          2 AKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQI
                                                                                                                                                                                                                                        Gaps
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spinal segmental nerve injury; chronic constriction injury; CCI;
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                                                                                                                                                                                                   Length 221;
                                                                                                                                                                                                                                      43; Indels
                                                                                                                                                                                                   48.9%; Score 540; DB 5; 52.7%; Pred. No. 1.3e-48; ive 45; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Protein P51153, SEQ ID NO 11024.
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21-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                  Query Match
Best Local Similarity 52...
Best Local 98; Conservative
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                                                                                                                                                                 Sequence 221 AA;
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claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal compania, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polynucleotides or their antibodies. The polynucleotide or the compound that the compound that it is useful for preparing a medicament for increating medicament as activity is useful for preparing a medicament for increasing pain and a scivity is useful for preparing a medicament for increasing medicament for increasing pain and a scivity is useful for preparing a medicament for increasing pain and a cativity is useful for preparing a medicament for irreating pain and a cativity is useful for preparing a medicament for irreating pain and a cativity is useful for preparing a medicament for irreating pain the parmaceutical composition comprising the one or more
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of The specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

88.1%; Score 532; DB 7; Length 203;
Best Local Similarity 47.6%; Pred. No. 8e-48;
Matches 100; Conservative 49; Mismatches 43; Indels 18; Gaps
or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMRASNELALAELEEEGKPEGPANSSKTC 210
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01-NOV-2001; 2001US-0346382P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 203 AA;
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, or human polynucleotides or a polynucleotide which represents a fragment, comprising the uncleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a crass or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity of one or more of the repression, a method for identifying a compound useful in treating especification, a method for identifying a compound useful in treating composition comprising the one or more of the specification, a method for identifying a compound useful in treating colypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating colypeptides or their antibodies. The polynucleotide or the compound comprising the modulates its activity is useful for preparing a medicament for treating colypeptides or their antibodies. The polynucleotide or the compound coliny (CCI) and spared nerve injury (SNI) in an animal (e.g. spin) colinity (CCI) and spared nerve injury (SNI) in an animal (e.g. spin) colinity is useful for preparing a medicament for treating colinity (CCI) and spared nerve injury (SNI) in an animal (e.g. spin) colinity by partined and partined for this patent did not form part of the printed condition) but was obtained in electronic form 
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47.6%; Pred. No. 8e-48;
ive 49; Mismatches 43; Indels
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                                                                                                                         Costigan M;
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                                                                                                                            Befort K,
                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 1017pp; English
26-NOV-2001; 2001US-0333347P.
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Matches 100; Conservative
                                                (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                            Woolf C, D'urso D,
                                                                                                                                                                       WPI; 2003-268312/26.
GENBANK; P51153.
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14-MAR-2001 (first entry)

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Lung cancer associated polypeptide sequence SEQ ID 534.
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associated proteins represented in AAB58106 - AAB58848. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective, cytostatic, cardioactive; and antagonists, machine neuroprotective; yulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial cativity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences. The lung cancer, chromosome cativity as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat diagnostic cardiovascular, renal, and proliferative discrders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and 44 MAKAYDHLFKLLLIGDSGVGKTCLIIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKIKLQ 103 61 IMDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQXILIG 120 121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180 cardioactive; immunomodulatory; muscular active; vulnerary; asstrointestinal; nephrotropic; antiinfective; synecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease. 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60 Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer. Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer 43; Indels 18; Gaps cancer associated protein; neuroprotective; cytostatic; characterisation of the polynucleotide and protein sequences Query Match

48.1%; Score 532; DB 3; Length 246;
Best Local Similarity 47.6%; Pred. No. 1.1e-47;
Matches 100; Conservative 49; Mismatches 43; Indels 1 181 RMRASNELALAELEEEGKPEGPANSSKTC 210 218 GRRSGN-----GNKP--PSTDLKTC 235 Claim 11; Page 1027-1028; 1425pp; English 08-MAR-2000; 2000WO-US005918. (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A. WPI; 2000-587514/55. N-PSDB; AAF18072. Sequence 246 AA; WO200055180-A2. 12-MAR-1999; Homo sapiens 21-SEP-2000 Ruben SM;

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STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                        US-08-824-873-4
                      3.396
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                                                                   March 15, 2004, 11:05:27 ; Search time 23 Seconds
   (without alignments)
   475.857 Million cell updates/sec
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Sequence 19,
Sequence 15,
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Sequence
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1 MAKQYDVLFRLLLIGDSGVG......LEBEEGKPEGPANSSKTCWC
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2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-51-55-35
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US-08-51-525-10
US-08-718-270A-10
US-08-718-270A-10
US-08-718-270A-10
US-08-916-901-3
US-08-916-901-8
US-08-916-901-8
US-08-916-901-8
US-08-511-525-14
US-08-531-525-14
US-08-531-525-14
US-08-531-525-14
US-08-718-270A-13
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US-08-531-525-51
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                                                                                                                                                                                                               389414 segs, 51625971 residues
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                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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430.5
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Best Local Similarity 52.9%; Pred: No. 2.4e-52; Matches 99; Conservative 45; Mismatches 43; Indels
                  US-09-255-920A-12

US-09-075-920A-13

US-09-075-920A-13

US-08-139-134-1

US-08-131-525-18

US-08-131-525-18

US-08-131-525-22

US-08-131-525-52

US-08-178-270A-52

US-08-178-270A-52

US-08-178-270A-52

US-08-178-270A-16

US-08-173-423-8

US-08-773-423-8

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,873
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0240 US
TELEPONMUICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08824873

Petent No. 5843717

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Guegler, Karl

TITLE OF INVENTION: NOVEL RAB PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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338.9
3377.6
3377.7
3377.7
338.0
338.0
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338.0
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123 ADEBOKROVGREGGGOLAKEYGMDFYETSACTNINIKESFTRLTELVLOAHRKELEGLRM 182
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                                                           61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW
                                     NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL
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                                                                                                                                                                                                                                                                                                          APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%; Score 527.5; DB 2; Length 205; 52.4%; Pred. No. 2.1e-50; ive 45; Mismatches 42; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: RECEDER, Donna M.
REGISTRATION NUMBER: 33,878
RESPERCE/DOCKET UNBER: 37-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     US-08-531-525-25; Sequence 25, Application US/08531525; Sequence 25, Application US/08531525; Patent No. 5840683; GENDERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 52.4%
Best Local Similarity 52.4%
Generative
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                                                                                                                                                           181 SPQGSNQ 187
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STATE: Colorado
COUNTRY: US
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STREET: 53
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                                                                                                                                                                                   61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                       61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
                                                                                                                                                             121 NKADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                             MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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; Pred. No. 2.4e-52;
45; Mismatches 43; Indels
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APPLICATION DATA:
APPLICATION NUMBER: US/00/***
FILING DATE:
CLASCY***
                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09198184
; Patent No. 6010859
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0240 US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.3%;
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Best Local Similarity 52.9%
Matches 99; Conservative
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MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                 181 SPQGSNQ 187
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CLONE: 234746
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61 IMDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWYSDVDEYAPEGVQKILIG 120
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                       123 ADEBQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTTFIS-IGIDFKIKTVELQGKKIKLQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                 Sequence 51, Application US/08531525
Patent No. 5840683
GENERAL INPORMATION:
APPLICANT: Placus, Matthew R.
APPLICANT: Abajian, Henry B.
APPLICANT: Rabajian, Henry B.
APPLICANT: Rode, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21.5EP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33.978
REFERENCE/POCKET NUMBER: 37-94
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.9%; Score 518.5; DB 2; 55.0%; Pred. No. 2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Greenlee and Winner, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 94; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colorado
                                                                                        183 RASNE 187
                                                                                                                               181 QGSNQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boulder
STATE: Colorad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-531-525-51
                                                                                                                                                                                                                   US-08-531-525-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIKAKMDKKLEGNSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQIW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            APPLICANT: Hlavka, Joseph J.
APPLICANT: Hlavka, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 5910-4781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 527.5; DB 2
; Pred. No. 2.1e-50;
45; Mismatches 42
                                                                                                                                                                                                Sequence 25, Application US/08718270A Patent No. 5910478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris
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Best Local Similarity 52.4%;
Matches 97; Conservative 49
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                        181 QGSNQ 185
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STATE: Colorado
                                            183 RASNE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino a STRANDEDNESS:
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ORGANISM:
US-08-718-270A-25
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CITY: Boulder
STATE: Colorado
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STREET: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTYDLLFKLLLIGDSGVGKTCYLFRFSDDAFNTTFIS-IGIDFKIKTVELQGKKIKLLQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NKADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLO 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: END FC compatible
CORPUTER: Floppy disk
COMPUTER: Floppy disk
APPLICATION NUMBER: US/08/718,270A
FLING DATE: 21-SEP-1996
FILING DATE: 21-SEP-1995
FILING DATE: 21-SEP-1995
FILING DATE: 21-SEP-1995
FILING DATE: 21-SEP-1995
ATPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATPLICATION NUMBER: US 60/004,091
                                                                                                                                                                                                           Peptidomimetics Inhibiting
the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                                                        3: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                 Sequence 51, Application US/08718270A Patent No. 5910478 GENERAL INFORMATION:
                                                                                    APPLICANT: HIAYKA, JOSEPh J.
APPLICANT: Pincus, Matthew R.
Phous, Malley John F.
APPLICANT: AD. 59104781e, John F.
APPLICANT: Kende, Andrew S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REPERENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                         TITLE OF INVENTION: Per
TITLE OF INVENTION: the
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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STATE: Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                            80303
                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-718-270A-51
.08-718-270A-51
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RESULT

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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: UNSURE
; LOCATION: (34)
; LOCATION: (34)
; OTHER INFORMATION: The xaa at position 34 represents an unknown amino
; OTHER INFORMATION: acid.
US-09-255-920A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: PETITE OF INVENTION: PETITE OF INVENTION: CF P21 Ras
CORRESPONDENCE 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 203;
...on US/09255920A
...ordation:
...ord: Fisher, Joseph
...ord: Fisher, Joseph
...ord: Applicant: Loorens, James
, Applicant: Luo, Ying
Applicant: Huang, Betty
, Applicant: Huang, Betty
, Applicant: Huang, Betty
, Applicant: Huang, Exol and Exo2, Exocytoric Proteins
, Tills OF Invention: Exol and Exo2,
, CURRENT Application Number: 60/0155,920A
, CURRENT FILING DATE: 1999-02-23
, PRIOR FILING DATE: 1998-02-23
, PRIOR FILING DATE: 1998-02-23
, PRIOR FILING DATE: 1998-02-23
, SOFTWARE: Patentin Ver. 6
, SOR IN NO 12
, LENGTH: 203
, TYPE: PRT

CURRENT: ENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPALIAL-
OPERATOR: PROFINE PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.7%; Score 515.5; DB 4; Best Local Similarity 56.0%; Pred. No. 4.4e-49; Matches 93; Conservative 41; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/08531525
Patent No. 5840683
GENERAL INFORMATION
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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Query Match
45.6%; Score 503.5; DB 2; Length 2
Best Local Similarity 46.4%; Pred. No. 9.8e-48;
Matches 96; Conservative 56; Mismatches 44; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ---NENSLQEAVDKIKSPPKKPSQKKK 198
                                       FILING DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
ALING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-531-525-10
; Sequence 10, Application US/08531525
; Patent No. 5840683
; GENERAL INPORMATION:
; APPLICANT: Hlavka, Joseph J.
; APPLICANT: Pincus, Matthew R.
; APPLICANT: No. 58406831e, John F.
; APPLICANT: Abalian, Henry B.
; APPLICANT: Kende, Andrew S.
                                                                                                                                                               NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Discopyge ommata
US-08-718-270A-35
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 DTAGQERFRIIT-AYYRGAMGIMKV-DITNEKSFDNIKNWIRNIEEHASSDVERMILGNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 ADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KTYDYLFKLLLIGDSGVGKTCLLFRFSEDAFNTTFISTIGIDFKIRTVELDGKKIKLQIW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.4%; Pred. No. 9.8e-48;
Matches 96; Conservative 56; Mismatches 44; Indels 11.
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APPLICANT: Hlavka, Joseph J.
APPLICANT: Bincus, Matthew R.
APPLICANT: Abajian, Henry B.
APPLICANT: Rende, Andrew S.
TITLE OF INVENTION: Peptidonimetics Inhibiting
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NENSLQEAVDKLKSPPKKPSQKKK 198
              APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIPRICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 37-94
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-6080
TELEPHONE: (303) 499-6089
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35, Application US/08718270A
Patent No. 5910478
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Discopyge ommata
US-08-531-525-35
                                                                                                                                                                                                                                                                                                             LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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62 DTAGGERFRIT-AYYRGAMGIMKV-DITNEKSFDNIKNWIRNIEEHASSDVERMILGNK 119
                                                                                                                                                                                                                                                                                63 DTAGOERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                             2 KTYDYLFKLLLIGDSGVGKTCLLFRFSEDAFNTTFISTIGIDFKIRTVELDGKKIKLQIW 61
                                                                                                                                        3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 CDMNEKROVSKERGEKLAIDYGIKFLETSAKSSINVEEAFITLARDIMTKLNKKM---
                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406811e, John F.
APPLICANT: No. 54406811e, John F.
APPLICANT: Rande, Andrew S.
APPLICANT: Rende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
DB 2; Length 207;
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72 AGOER-RTITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -EEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLOAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 YDYLIKLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIMDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: Abajian; John F.
APPLICANT: Kende, Andrew S.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 MDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVEEVFFSIG--
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.e-46;
54;
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CURRENT APPLICATION DATE:
APPLICATION UNMER: US/08/531,525
PILING DATE: 21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 ASNELALAE-----LEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 LSDTDSRAEPATIKISQTDQAAGAGQATQKSAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

44.8%; Score 494.5;
Best Local Similarity 46.9%; Pred. No. 1e-4
Matches 100; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
               PRICR APPLICATION DATA:

APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/SEBVI INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-95
TELEPHONE: (303) 499-8089
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Alinear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5840683
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Arabidopsis thaliana
US-08-718-270A-10
  21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 YDYLIKLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIMDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
44.8%; Score 494.5; DB 2; Length 215;
Best Local Similarity 46.9%; Pred. No. 1e-46;
Matches 100; Conservative 40; Mismatches 54; Indels 19; Gaps
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the Oncogenic Action of P21 Ras
52
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 ASNELALAE----LEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hlavka, Joseph J.
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08718270A
Patent No. 5910478
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                     NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             TELEPHONE: (303) 499-8080
TELEPAX: (303) 499-8080
TELEPAX: (303) 499-8080
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 215 amino acids
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colorado
: US
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ORGANISM: Are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 80303
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Gaps

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61 QIWDTAGQERFHTIT-SYYRGAMGIMLVYDITNAKSFENISKWLRNIDEHANEDVERMLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GNK-DMEDKRVVLKSKGQ--IAEHAIRFPETSAKANINIEKAFLTLAEDILQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GNKADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLO 171
                                                                                                                                                                                                                                                                                                                                                                                               Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                             44.2%; Score 488.5; DB 2; 55.8%; Pred. No. 4.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: PESECBG (TO Windows Version 2.0
CURTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
RIGHT APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08916901
Patent No. 5892012
PAPELICANT: Hillman, Jennifer L. APPLICANT: Lal, Freeti
APPLICANT: Caller, Neel C. APPLICANT: Calley, Neil C. APPLICANT: Shah, Purvi
ITTLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                REPERENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEFANS: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGIGSTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
  33,878
                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Discopyge ommata
US-08-718-270A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                            194 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             single
                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-916-901-3
                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAXKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTTFISTIGIDFKIKTVELHGKKIKL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GNK-DMEDKRVVLKSKGQ--IAEHAIRFFETSAKANINIEKAFLTLAEDILQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                      44.2%; Score 488.5; DB 2; Length 194; 55.8%; Pred. No. 4.1e-46; tive 41; Mismatches 30; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Polos Sudvale, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION 213.

PRIOR APPLICATION NUMBER: US 08/531,525

FILING DATE: 21-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/004,091

FILING DATE: 21-SEP-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/08718270A
Patent No. 5910478
GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
                NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                       Discopyge ommata
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.8%
Matches 96; Conservative
                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boulder
STATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Die
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-718-270A-34
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                                                                                                                                                                                                                                                     1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                             5; Gaps
                                                                                                                                                        Length 201;
                                                                                                                                                                                           64; Indels
                                                                                                                                                  Query Match
43.3%; Score 478.5; DB 2;
Best Local Similarity 45.0%; Pred. No. 5.5e-45;
Matches 91; Conservative 42; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF-0367 US
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
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PRIOR DATA:
APPLICATION NUMBER: 08/916,901
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367
TELECOMMUNICATION INFORMATION:
TELEPHON: 415-855-055
INFORMATION FOR SEC ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : : : | | | | 176 GAASGGERPNLKIDSTPVKPAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 RMRASNELALAELEEEEGKPEG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09154602
Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDRESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LIVRTUT04
; TYPE: amino acid
; STRANDEDRES: single
; TOPOLOGY: linear
; INMMEDIATE SOURCE:
; LIBBARY: LIVRUT04
; CLONE: 2514506
US-08-916-901-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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IS-09-154-602-3
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61 IMDTAGOERYOTITKOYYRRAOGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                             61 IWDTAGGERFRIITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVG 120
                                                                                                                                                                                                                       121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                              1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                 Gaps
                                                                  2,
                                     DB 4; Length 201;
                                                                  64; Indels
                                   43.3%; Score 478.5; DB 4
45.0%; Pred. No. 5.5e-45;
ative 42; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                              Search completed: March 15, 2004, 11:09:10 Job time: 23 secs
                                                                                                                                                                                                                                                                                                          181 RMRASNELALAELEEEEGKPEG 202
                                     Query Match
Best Local Similarity 45.09
Matches 91; Conservative
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US-09-154-602-3
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1 MAKQYDVLPRLLLIGDSGVG.....LEEEEGKPEGPANSSKTCWC
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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                                                                                                                                                                                           March 15, 2004, 11:08:07; Search time 34 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       809742 segs, 211153259 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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10:
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2, Appli Sequence 701, App Sequence 4, Appli Sequence 4997, Ap Sequence 2497, Ap Sequence 234, App Sequence 1571, Ap Sequence 1571, Ap Sequence 8, Appli Sequence 8, Appli Sequence 6000, Ap Sequence 6000, Ap Sequence 6, Appli Sequence 5076, App Sequence 5076, App	
(I	US-09-817-198A-2 US-09-817-198A-5 US-09-817-198A-5 US-09-817-198A-4 US-09-764-868-1120 US-09-764-868-1120 US-09-925-304-937 US-09-925-306-1571 US-09-925-306-1571 US-09-925-306-1571 US-09-925-306-1571 US-09-128-714-3241 US-10-128-714-8600 US-10-128-714-8600 US-10-128-714-8600 US-10-128-714-8600 US-10-128-714-8600 US-10-128-714-8600 US-10-128-714-8600	
DB	   0000044400   44410	
% Query Aatch Length DB	2018 2018 2018 2018 2018 2007 2007 2006 1001	
% Query Match	1000.0 908.8 908.8 907.5 707.5 707.5 80.0 80.0 80.0 80.0 80.0 80.0 80.0 80	
Score	1105 1105 1105 1002 1002 833 530 530 523 523 523 523 523 523	
Result No.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	

Sequence 766, App Sequence 3, Appli Sequence 193, App Sequence 6261, App Sequence 6261, App Sequence 21876, App Sequence 17300, App Sequence 1730, App Sequence 1737, App Sequence 1707, App Sequence 1707, App Sequence 150, Appli Sequence 16, Appli Sequence 18, Appli Sequence 18, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1106, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 1138,	Seguence 67, Appl Seguence 67, Appl
9 US-09-834-765-766 9 US-09-967-736-3 14 US-10-10291-1023 15 US-10-10291-1023 16 US-10-369-493-6261 17 US-10-369-493-6261 18 US-10-369-493-6261 19 US-09-967-736-8 10 US-09-967-736-8 10 US-09-967-736-8 10 US-09-967-736-8 11 US-10-369-493-1787 12 US-10-369-493-1787 13 US-09-975-150 14 US-10-369-493-1787 15 US-09-975-150 16 US-09-975-160 17 US-09-976-173-189 18 US-09-976-173-189 19 US-09-976-173-189 10 US-09-976-173-189 10 US-09-976-173-189 10 US-09-976-173-189 10 US-09-976-173-189 11 US-10-108-260A-4746 12 US-09-817-199A-4 13 US-09-764-868-684 14 US-10-369-493-501 15 US-09-764-868-684 16 US-09-764-868-1106 17 US-09-764-868-1106 18 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1106 19 US-09-764-868-1107-1	9 US-09-350-874-67 14 US-10-106-989-67
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## ALIGNMENTS

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     Sequence 2, Application US/09817198A

Patent No. US20020146758A1

GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CLO01188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL
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                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1105; DB 9; Length 212; 100.0%; Pred. No. 2.2e-106; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 212; Conservative
                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                         US-09-817-198A-2
US-09-817-198A-2
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NAME/KEY: SITE
LOCATION: (139)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                    121 NKADEBOKROVGREGGG-----QLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHR 174
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REPERENCE: CLO01188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT APPLICATION NUMBER: US/09/817,198A
SOFTWAREN FILING DATE: 2001-03-27
SOFTWARE: FRELSE for Windows Version 4.0
SEQ ID NOS: 33
SOFTWARE: FRELSE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNBFHSSHISTIGVDFKVKTIBVDGIKVRIQ
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1120
LENGTH: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBACE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                        175 KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC 212
                                                                                                                                                                                               181 KELEGLRWRASNELALAELEEEEGKPEGPANSSKTCWC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
97.5%; Score 1077; DB 9;
Best Local Similarity 97.6%; Pred. No. 1.8e-103;
Matches 207; Conservative 2; Mismatches 3;
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Sequence 1120, Application US/09764868

Sequence 1120, Application US/09764868

Patent No. US/20020168/11A1

GENERAL INFORMATION:
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Patent No. US20020146758A1
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ORGANISM: Rattus norvegicus
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ORGANISM: Homo sapiens
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US-09-817-198A-4
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Patent No. US20020146758A1
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: OF UGLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: OF UGLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOO1188
FILE REFERENCE: CLOO1188
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
CURRENT FILING DATE: SOO1-03-27
NUMBER OF SEQ ID NOS: 33
ENGINE SEQ ID NO 5
LENGTH: 218
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                                                                                                                                        Sequence 701, Application US/09764868

Fatent No. US20020168711A1

GENERAL INFORMATION:

APPLICANT ROSen et al.

TITLE OF INVENTION:

FILE REFERENCE: PTZ32

CURRENT FILING DATE: 2001-01-77

Prior application data removed - refer to PALM or file wrapper; NUMBER OF SEQ ID NOS: 1510

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 701

LENGTH: 401
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Pred. No. 5.2e-105;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1105; DB 9; Best Local Similarity 100.0%; Pred. No. 5.4e-106; Matches 212; Conservative 0; Mismatches 0;
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                       181 RMRASNELALAELEEEGKPEGPANSSKTCWC 212
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Best Local Similarity 97.2%;
Matches 212; Conservative
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; ORGANISM: Homo sapiens
US-09-764-868-701
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ORGANISM: Homo sapiens
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US-09-925-302-534
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Fublication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION UNMER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 4997
LENGTH: 224
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                     LOCATION: (161)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                       LOCATION: (188)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                       LOCATION: (151)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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75.3%; Score 832; DB 9; Length 188;
Best Local Similarity 97.6%; Pred. No. 3.9e-78;
Matches 160; Conservative 0; Mismatches 4; Indels
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; ORGANISM: Caenorhabditis elegans
US-10-369-493-4997
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                                                                          NAME/KEY: SITE
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RESULT.

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LENGTH: 206
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                                                                                                                                                                                                                                                                                                                  61 IMDTAGQERYQTITKQYYRRAQGIPLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                               1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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48.0%; Score 530.5; DB 9; Length 218;
Best Local Similarity 55.8%; Pred. No. 9.2e-47;
Matches 96; Conservative 46; Mismatches 29; Indels 1
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Sequence 1571, Application US/09925300

Patent No. US2020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben,

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT APPLICATION NUMBER: PCT/US00/05988

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 1899

SOFTWARE: PatentIn Ver. 2.0

SEC ID NO 1571
                                                                                                                                   Length 246;
                                                                                                                                   Query Match
48.1%; Score 532; DB 9; Length 24
Best Local Similarity 47.6%; Pred. No. 7.6e-47;
Matches 100; Conservative 49; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 RMRASNELALAELEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 GRRSGN-----GNKP--PSTDLKTC 235
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 534
LENGTH: 246
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CORGANISM: Homo sapiens
US-09-925-300-1571
                                                                            ORGANISM: Homo sapiens
US-09-925-302-534
                                                            TYPE: PRT
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Sequence 8, Application US/09794257 Patent No. US20020009804A1 GENERAL INFORMATION:

US-09-794-257-8

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General information:

General information:

APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Low Inversion Methods of Use
FILE OF INVENTION: Methods of Use
FILE OF INVENTION NUMBER: US 60/285,697
FRIOR APPLICATION NUMBER: US 60/285,697
FRIOR APPLICATION NUMBER: US 60/285,890
FRIOR APPLICATION NUMBER: US 60/303,899
FRIOR FILING DATE: 2001-06-05
FRIOR APPLICATION NUMBER: US 60/316,362
FRIOR APPLICANTON NUMBER: US 60/316,362
FRIOR APPLICATION NUMBER: US 60/316,362
FRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFFWARE PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804Alel TITLE OF INVENTION: Human G-Proteins FILE REFERENCE: 35800/209285 CURRENT APPLICATION NUMBER: US/09/794,257 CURRENT APPLICATION NUMBER: 05/09/794,257 PRIOR APPLICATION NUMBER: 60/185,606 PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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58.7%; Pred. No. 5.1e-46;
tive 31; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Aspergillus fumigatus
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Matches 98; Conservative
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Best Local Similarity 54.03
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: homo sapiens
US-09-794-257-8
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APPLICANT: Goo, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5202)
CURRENT APPLICATION NUMBER: US / 10/369, 493
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MARRPYDMLFKLLLIGDSGVGKTCILYRFSDDAFNTTFISTIGIDFKIKTIELKGKKIKL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.5%; Score 514; DB 14;
46.9%; Pred. No. 4.2e-45;
iive 48; Mismatches 51;
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46.5%; Score 514; DB 15;
Best Local Similarity 46.9%; Pred. No. 4.2e-45;
Matches 100; Conservative 48; Mismatches 51;
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US-10-179-766-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 46.99
Matches 100; Conservative
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Publication No. US20030119013A1

GENERAL INFORMATION:

APPLICANT: Janay, Bo

APPLICANT: Taiknoff, Daniel

APPLICANT: Taiknoff, Daniel

APPLICANT: Taiknoff, Daniel

APPLICANT: Lenieux, Sebastien M

APPLICANT: Lenieux, Sebastien M

APPLICANT: Lenieux, Sebastien M

APPLICANT: Lenieux, Sebastien M

TITLE OF INVENTION: Methods of Use

FILE REPERBENCE: 10182-018-99

FILE REPERBENCE: 10182-018-99

FILE REPERBENCE: 10182-018-99

FRIOR APPLICATION NUMBER: US 60/285,697

FRIOR APPLICATION NUMBER: US 60/285,697

FRIOR APPLICATION NUMBER: US 60/285,890

FRIOR APPLICATION NUMBER: US 60/285,890

FRIOR PLING DATE: 2001-04-27

FRIOR PLING DATE: 2001-04-27

FRIOR FILING DATE: 2001-04-27

FRIOR FILING DATE: 2001-06-05

FRIOR PRICATION NUMBER: US 60/303,899

FRIOR PLILNG DATE: 2001-07-09

FRIOR FILING DAT
                                                                                                                      65 DTAGOERFRIITTAYYRGAMGILLVYDVTDERSFONIRTWFSNVEOHASEGVHKILIGNK 124
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5 RNYDFLIKLLLIGDSGVGKSCCLLRFSEDSFTPSFITTIGIDFKIRTIELDGKRVKLQIW 64
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58.7%; Pred. No. 5.1e-46;
tive 31; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10179766 Publication No. US20030190312A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garigan, Delia
Hsu, Ao-Lin A.
Lehrer-Graiwer, Josh
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Best Local Similarity 58.7%
Matches 98; Conservative
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APPLICANT: Apfeld, Javier
APPLICANT: Dillin, Andrew
APPLICANT: Garigan, Delia
APPLICANT: Hsu, Ao-Lin A.
APPLICANT: Lehrer-Graiwer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Aspergillus
US-10-128-714-8600
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GENERAL INFORMATION:

APPLICANT: ZHU, Shiaoping et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

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-MODEL=frame+ p2n.model -DEV=xlp
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-Cgn2_1/USPTO_spool_p/US09817198/runat_15032004_101746_20542/app_query.fasta_1.391
-DE-Cgn2_1/USPTO_spool_p/US09817198/runat_15032004_101746_20542/app_query.fasta_1.391
-DE-CGN2_10-10FWT=fastap -SUFFIX=xge -MINMATCH=0.1.-LCOPCT=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=0-ALIGH=15 -MODE=LOCAL
-UNITS=bits -NORM=ext -HEAFSIZE=560 -MINLEN=0 -MAXIEN=200000000
-USER=US09817198 @CGN 1 1 5265 @runat_15032004_101746_20542 -NCPU=6 -ICPU=3
-NO MMAP -LARREQUERY -NGG SCORES=0 -MATY -DSPBEADCK=100 -LONGIAG
-DSW TIMEOUT=120 -WARN TNECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                GenCore version 5.1.6
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
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Email: cgapbs-r@mail.nih.gov
Tissaue Procurement: Jeffreg Aren M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
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Web site: http://www.nisc.nih.gov/
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                         GluGlyProAlaAsnSerSerLysThrCysTrpCys 212
                                                                                                                                                                                                                                                                                                                                                                                681 GAGGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGC 716
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Strausberg, R.
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                                              PAT 06-JUN-2002
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Patent: WO 0218424-A 74 07-MAR-2002;
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                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Sequence 74 from Patent WO0218424.
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                                                                                                                                                                                                                                                                                                                                                                                                                  ROD 27-APR-1993
                                                                                                                                                                                                                         181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGluGlyLysPro 200
 121 ABniyBAlaAspGluGluGlnLy8ArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                         LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                          628 AAGGAGTACGGCATGGACTTCTACGAAACAAGTGCCTGCACCAACCTTAATATTAAAGAG 687
                                                                                                                                               SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Original source text: Rattus norvegicus (strain Sprague-Dawley)
(library: LAMBDA ZAPII) adult brain cDNA to mRNA.
Location/Qualifiers
                       Elferink, L.A., Anzai, K. and Scheller, R.H.
rabls, a novel low molecular weight GTP-binding protein
specifically expressed in rat brain
J. Biol. Chem. 267 (9), 5768-5775 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                      катканыбх 945 bp mRNA linear RC
Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds.
M83679
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LMW GTP-binding protein.
Rattus norvegicus (Norway
Rattus norvegicus
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RATRAB15X
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                                                                                                                                                                                                                                         /db_xrefe="taxon:10090"
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                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 55 Row: d Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19527265. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 ATGGCGAAACAGTACGATGTGCTGTTCCGGCTACTGCTGATCGGGGGACTCCGGGGGTTGGC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 AAGACATGCCTGCTGTGCCGCTTCACCGACAAGGAGTTCCACTCCTCGCATATCTCCACC 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCAGGGAATATTTTTAGTCTACGACATTAGCAGTGAGCGCTCCTATCAGCATATCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L..
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetalaLyaGlnTyrAspValLeuPheArgLeuLeulleGlyAspSerGlyValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229. .720
/note="RAB; Region: Rab subfamily of small GTPases"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                           note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                      CGAP_Mam6"
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                                                                                                                                                                                                                                                                                                                                      lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                gene="Rab15"
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1090.00
99.53$
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98.64$
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UNIH-MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced gi:26251822.
Ontact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
TobnA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
Toshiyuki and Piero Carninci (RIKEN)
Toshiyuki and Piero Carninci (RIKEN)
Toshiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@bcgsc.Dc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readdan Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saedein, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorrie, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
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Location/Qualifiers
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="RAB; Region: Rab subfamily of small GTPases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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82.42%
82.42%
94.89%
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Strausberg, R.
Direct Submission
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                                                                                                                                                                                                                                                   PUBMED
REFERENCE
AUTHORS
TITLE
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COMMENT
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Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G. M., Hong, L.,

Scheefz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Morkernan, K. J., Mallaky, S. J., Bosak, S. A., McRawa, P. J.,

Morley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCG40679 3326 bp mRNA linear PRI 11-DEC-2003
Homo sapiens RAB15, member RAS onocogene family, mRNA (cDNA clone
MGC:42319 IMAGE:4817835), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 ATCGGTGTTGACTTTAAGATGAAAACCATCGAAGTAGACGCCATCAAAGTGAGGATACAG 399
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                                                                                                             280, AAGACCTGCCTGCTATGCCGCTTCACCGACAACGAGTTCCACTCCTCGCATATCTCCACC 339
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetalaLysGlnTyrAspValLeuPheArgLeuLeuLeuleGlyAspSerGlyValGly
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altachul, S.P., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soarse, W.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McZwan, P.J.,
McKernan, K.J., Malek, J.A., Gunarathe, P.H., Richards, S.W.,
Vilalon, D.K., Malek, J.A., Garei, P.H., Richards, S.W.,
Vilalon, D.K., Walk, M.S., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Schumod, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Becketrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McClowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-DEC-2003) National Institutes of Health, Xenopus Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4801, Rockville, MD 20892-7510, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="MGC:68722 IMAGE:4057038"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-r@mail.nih.gov
Tissus Procurement: Dr. Igor Dawid
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/db_xref="taxon:8355"
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Klein, S. and Strausberg, R.
   (bases 1 to 2348)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleLeuIleGlyAsnLysAlaAspGluGluGluGlnLysArgGlnValGlyArgGluGlnGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                664 CTGGAAGGCCTCCGGATGCGTGCCAGCAATGAGTTGGCACTGGCAGTGGCAGGAGGAG 723
                                                                                                                                                                                                              65 AAGACCTGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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                                                                                                                                                                                                                                                                                                                                                 ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 GGGTGCCTCACCGGGGAAGGCAAGGCGAGGGCCAGATGGGAAGGCAAATGCTTCCAGGAA 423
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.
1 (bases 1 to 2348)
Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W. and Richardson,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRT 09-DEC-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 GCTTTGCCTTCCACAGCCCTGGATGAAGACCTCTGGTACGCACCAGAAGGCGTCCAGAAG
                                                         MetAlaLysGlnTyrAspValLeuPheArgLeuLeuIleGlyAspSerGlyValGly
                                                                                                                   5 ATGCCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGC
                                                                                                                                                                             LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 AAGTGGGTCAGTGACGTGGATGA-GGTAGGAGATGCCACCTCACTGCCGGGGTGTGGAGA
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Xenopus laevis cDNA clone MGC:68722 IMAGE:4057038,
BC063736
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US-09-817-198C-2 (1-212) x BC040679 (1-3326)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2560)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buterow, K.H., Ronze, T., Wang, J., Haich, F., Diatchenko, L., Maruslna, R., Parmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bornaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Mulaky, J.A., Gunarane, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Ketteman, M., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Katyyinski, M., Touchman, J.W., Green, E.D., Butterfield, Y.S., Kazyyinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Manna, and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna and manna
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/clone="MGC:6897 IMAGE:2655151"
/tissue type="Mammary tumor: MMTV-LTR/INT3 model. 5 month old mouse. Taken by biopsy."
/clone lib="NGT GAAP_Mam2"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: i Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19527265. Location/Qualifiers
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Direct Submission
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Direct Submission
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Gene (14-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Email: cgapbs-r@mail.nih.gov
Thsue Procurement: Gilbert Smith, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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12477932
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/db_xref="LocusID:104886"
/db_xref="MGI:1916865"
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/mol_type="mRNA"
/strain="FVB/N-3"
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/product="Rab15 protein"
/protein_id="AAH13790.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA
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ORGANISM
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JOURNAL
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                                                                                      REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159. .551
/note="RAB; Region: Rab subfamily of small GTPases"
/db_xref="CDD:cd00154"
     ASDVDEYAPDGVQKILIGNKADEEQKRQVGKNQGLKAMFKH"
                                                                                                                                                                                                       2348
134
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20
15
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
                                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                               Alignment Scores:
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SOURCE
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sequenced by GBF (National Research Centre for Biotechnology Ltd., Braumschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone DKPZp686J06205) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="human fetal brain"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH108; sites SfiIA + SfiIB"
/dev stage="fetal"
1. .2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="CPRPOGGRNCOPIRLEAVAPEAGVRDKSRGVDFKMKTIEVDGIK
VRIQIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEVGDATS
LPGCGEGASPGKARRGPDGKANASRKLCLPQPWMKTSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similarity to GTP-binding protein rabl5 (Rattus norvegicus)"
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="CAB45901.1"
/db_xref="GI:34365091"
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                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="14q23.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-817-198C-2 (1-212) x HSM806937 (1-2210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="DKFZp686J06205"
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Номо sapiens mRNA; cDNA DKFZp686J06205 (from clone DKFZp686J06205).
BX640825
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(bases 1 to 2210)

Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wilmann, S.

The German Human cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 ATCGGTGTTGACTTTAAGATGAAGACTATCGATGTAGACGCCATCAAAGTGAGAATACAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaGlnGlyllePheLeuValTyrAspileSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 AAGTGGGTCAGTGGATGAGTACGCTCCAGAAGGAGTCCAGAAGATCCTAATTGGG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnLysAlaAspGluGluGluLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCGAAACAGTACGATGTGCTGTTCCGGCTACTGCTGATCGGGGACTCCGGGGTTGGC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         514 AATAAGGCTGATGAAGAGCAGAACGGCAGGTGGGGAGAGAACCAGGGGCAGCTGGCT 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGACATGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCATATCTCCACC
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/note="RAB; Region: Rab subfamily of small GTPases"
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            db_xref="GI:15489394"
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MEDLINE 22388257  PUBMED 12477932  REFERENCE 2 (bases 1 to 1726)  AUTHORS Strausberg,R.  TITLE Direct Submission JOURNAL Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Lin.at: http://image.llnl.gov Series: IRAK Plate: 117 Row: g Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.  FEATURES  1. 1726  Amol type="MRNA" (db Xref="taxon:7955" (clone="MRNA" (db Xref="taxon:7955" (clone="MGC:64010 IMAGE:6792909" (clone="MGC:64010 IMAGE:6792909" (clone="MGC:64010 IMAGE:6792909" (clone="MGC:64010 IMAGE:6792909" (clone="MGC:64010 IMAGE:6792909" (clone="MGC:64010 IMAGE:6792909" (clone="MGC:64010 IMAGE:6792909") (clone="MGC:64010 IMAGE:6792909")	/lab_host="DH10B"	Alignment Scores:
Db         508 ATGAATTAGTTCCAAGTCTTCCCTGTGAGCAGCTTCTTTCCTGAAATCTTGGGACCAGGT 567           Qy         107	107	snLeu       ysglu       AGGAG		AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klaubner, R.B., Collins, F.S., Wagner, L., Shanemer, C.M., Schuler, G.D., Altachul, S.F., Zeeberg, B., Buetcow, K. H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownsfelm, M.J., Usdin, T.B., Toshiyuki, S., Carinici, P., Frange, C., Raha, S.S., Loquellano, M.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Ganzatne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Murny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

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/db_xref="G1:2317272"
/translation="MAKKTYDLLPKLLLIGDSGVGKTCILFRFSDDAFTSTFISTIGI
DFYRATISTRGKKIKLOYDTAGGPRFHITTSYYRGAMGIMLVYDITNEKSFENIVK
WLRNIDEHANEDVERAVILGNKCDMTDKRVVNKERGEAJAREHGIRFMETSAKSNINIE
RAFCELAEAILDKTSGRESAENQERVIIDRRNQEKAPGYSKCCA"
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopterrygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Best Local Similarity:
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               GTCTGGGACACAGGAGGAGAGAGGTTTAAGACCATCACCACTGCATACTACAGAGGG
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster mRNA for Rab10, complete cds.
AB006189
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Rab proteins of Drosophila melanogaster: novel
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1.1613
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AF498943 624 bp mRNA linear PRI 01-MAY-2002
Homo sapiens small GTP binding protein RAB8 (RAB8) mRNA, complete
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FKIRTIELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNW
100 MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle 119
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Catarrhini, Hominidae; Homo.
                                                                                                                                                                                          2 (bases 1 to 624)
Puhl, H.L. III, Ikeda, S.R. and Aronstam, R.S.
Direct Submission
Submitted (05-APR-2002) CDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA
Location/Qualifiers
                                                                      60 GinileTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrArg
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc
1 (bases 1 to 624)
Puhl, H.L. III, Ikeda, S.R. and Aronstam, R.S.
Homo sapiens RAB family small GTP binding protein RAB8
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/protein_id="AAM21091.1"
/db_xref="GI:20379062"
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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MAKKTYDLLFKLLLIGDSGVGKTCILFRFSDDAFTSTFISTIGI
DEKTKTVELEGKKIKLOIMDTAGQBRFHTITTSYRGAMGINLYDITNBKSFENIYK
MLRNIDEHANEDVEMILGNKCDWTDKRVVNKERGBALAREHGIRFMETSAKSNINIE
RAFCELABALLDKTSGRESARNQERVIIDRRNQEKAPGYSKCCA"
                        Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Liw, C., Lewis, S. E., Rubin, G. M. and Celniker, S.
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                                                                                                                                                           Submitted (19-00T-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
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Matches:
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/db_xref="G1:16648398"
/db_xref="FLYBASE:FBgn0015789"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="19C1-19C1"
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Location/Qualifiers
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gene="Rab10"
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1 (bases 1 to 624)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundiny,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Parmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
IRNIEEHASADVEKMILGNKCDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVEN
AFFTLARDIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFPRCVLL"
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Matches:
Conservative:
Mismatches:
Indels:
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Homo sapiens mel transforming oncogene
NK14)- RABB homolog mRNA, complete cds.
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Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Direct Submitsion

M. Submitted (13-MAY-2001) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length repression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.

Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="mel transforming oncogene (derived from cell line NKI4)- RAB8 homolog"
/protein_id="AAP35848.1"
/db_xref="G1:3058320"
/translation="MAKTYDYLFKLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGID RYRTFILEDGKIKLQIMPTAGQERFRITTAYYRGAMGIMLYVDITNEKSFDNIRNW IRNIERHSAADVERGHIGHKCDYNDKRQVSKERGEKLALDYGIKFMETSAKANINVEN AFFTLARDIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFPRCVLL"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 660)
Zahraoui,A., Joberty,G., Arpin,M., Fontaine,J.J., Hellio,R., Tavitian,A. and Louvard,D.
A small rate Grpese is distributed in cytoplasmic vesicles in non polarized cells but colocalizes with the tight junction marker ZO-1 in polarized epithelial cells
J. Cell Biol. 124 (1-2), 101-115 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnlleLysGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 AlaGlnGlyIlePheLeuValTyrAspileSerSerGluArgSerTyrGlnHisileMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                 241 GCAATGGGCATCATGCTGGTCTACGACATCACCAAGAAGTCCTTGACAACAACTGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 LysirpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                                                                                                                                                                                                                                                                                             21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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rab-related GTP-binding protein.
Homo sapiens (human)
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                                                   1.1e-44
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                                                                                                                  Best Local Similarity:
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                                                                                               Percent Similarity:
                                     Alignment Scores:
Pred. No.:
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DB:
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Za (bases 1 to 624)

Ralnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Kalnine, N., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Roundinya, M. and Farmer, A.

Direct Submission

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Lag). The CDS has been directionally cloned using BD in-Fusion (TW)

cloning system between the Sall and Hindli sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site

and before 'ATG' to provide Kozak consensus sequence,' GG' after

last codon and before Hindli site to maintain reading frame.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="waktyoylfkilligosgygktcvifrfseddafnstfstigid
Fkirtieldgkrikloiwdtaggerfrtittayyrgamgimlvyditneksfdnirnw
irnieehasadveknilgnkcdvndkrqvskergeklaldygikfmetsakaninven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic construct synthetic construct synthetic construct artificial sequences.

I (bases 1 to 624)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Chening of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cransT_table=11
/product="Homo sapiens mel transforming oncogene (derived
from call line NK4). RABB homolog"
/protein id="AAP36967.1"
/db_xref="GI:30585389"
                                                                                                                                                                                                                                                                                                                                                           SYN 13-MAY-2003
oncogene (derived
                                                                            141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                      480
                                                                                                                                                           161 SerpheThrArgieuThrGluLeuValLeuGlnAlaHisArgiysGluLeuGluGlyLeu 180
                                                                                                                                                                                                   540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="GH00783L1.0"
/clone_lib="BD Creator(TM) CDS Library derived from MGC
                                                                                                                                                                                AsniysAlaAspGluGluGlniysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla
                                                                                                     :::||||||:::||||421 CTCGACTAGGAGACCAGCGGGAGACACACATGAAAAT
                      AFFTLARDIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFFRCVLLL"
                                                                                                                                                                                                                                                                                                                                                                                Synthetic construct Homo sapiens mel transforming onc
from cell line NK14)- RAB8 homolog mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                 linear
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/note="Vector: pDNR-Dual"
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note="Mutations: 623:Stop->Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="synthetic construct"
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/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                               mRNA
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trans1 table=
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PRI 08-MAR-1994

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/tränslation="MAKTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGID
KIRTIELGREKRIKLQIWDTAGGERFRTITTATXFGAMGIMUTWYDITNEKSFDNIRNW
IRNIEEHASADVERGHILGHKCDVWDKRQVSFERGEKLALDYGIKFWFSAKANINVEN
AFFTLARDIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFFRCVLL"
                                                                                                                                                        gene family
                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                                                                                                                                               Chavrier, P., Vingron, M., Sander, C., Simons, K. and Zerial, M. Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (17-AUG-1990) Zerial M., EMBL, Meyerhofstrasse 1,
                                                                                                                                                          protein transport; ras gene; ras
                                                                                      760 bp mRNA linear M
rab8 mRNA for ras-related GTP-binding protein.
                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760
999
445
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Matches:
Conservative:
Mismatches:
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/function="GTP binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .760
/organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GOA:P24407"
/db_xref="SWISS-PROT:P24407"
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/db_xref="G1:6006436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="mRNA"
/strain="cocker spaniel"
/db_xref="taxon:9615"
/clone="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-817-198C-2 (1-212) x CFRAB8 (1-760)
                  571
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1. .760
/gene="rab8"
551 AGCCCCCAGGGGAGCAACCAG
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GTP-binding protein; p
Canis familiaris (dog)
Canis familiaris
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                                                     RESULT 15
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                                                                                                                                                                                                                                                             /product="rab8 small GTP binding protein"
/protein id="CAA40065.1"
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/db_xref="G0A:124407"
/db_xref="SWISS-PROT:P24407"
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/db_xref="SWISS-PROT:P24407"
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IRNIEBHASADVERVILGNECDYNDRRQVSRERGEKTALDYGIKFWETSAKANINVEN
AFFTLARDIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFPRCVLL"
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                  Direct Submission
Submitted (26-NOV-1990) A. Zahraoui, INSERM-U 248, 10 AVENUE
VERDUM, 750-10 PARIS, FRANCE
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="Human pheochromocytoma cDNA library"
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Wehrman T;
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Wang D, Liu C, Drmanac RT,
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-DGV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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19-MAY-2000; 2
07-JUN-2000; 3
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24-FEB-2000;
02-MAR-2000;
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30-JUN-2000;
07-JUL-2000;
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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17-MAR-2000;
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                                                                                                                                                                            AAS27053;
                                                                                                                                   AAS27053
                                                                                                                  RESULT
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                                                                                                                                          The invention relates to an isolated polynuclectide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

(I) and (III) are useful for diagnostic evaluation of disorders.
(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200
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                                       New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AAGACCTGCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleTrpAspThrAlaGlvGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAG
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 1054 BP; 240 A; 314 C; 304 G; 195 T; 0 U; 1 Other;
                                                                                                                  Claim 22; SEQ ID NO 74; 284pp + Sequence Listing; English
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Matches:
Conservative:
Mismatches:
Indels:
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100.00%
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WPI; 2002-583321/62
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               P-PSDB; ABP62882
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antilificammatory; anti-HIV, antibacterial; antilificammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis; inflammatory condition; organ transplant rejection; infection; hepatitis; disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.
                                                      181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysPro 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
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                                                                                                                                                                                                                                                                          681 GAGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGC 716
                                                                                                                                                                                                              201 GluGlyProAlaAsnSerSerLysThrCysTrpCys 212
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2000US-0229343P.
2000US-02293144P.
2000US-0229513P.
2000US-0229513P.
2000US-0239513P.
2000US-0231243P.
2000US-0231244P.
2000US-023164P.
2000US-023239P.
2000US-023239P.
2000US-023239P.
2000US-0232497P.
2000US-023493P.
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2000US-0241786P.
2000US-0241786P.
2000US-0241808P.
2000US-0241803P.
2000US-0241803P.
2000US-02418126P.
2000US-0241817P.
2000US-0244617P.
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2000US-0237037P.
2000US-0237038P.
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2000US-0239935P.
2000US-0239937P.
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     01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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21-SEP-2000;
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17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249269P.
17-NOV-2000; 2000US-0249269P.
01-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025186P.
06-DEC-2000; 2000US-025186P.
06-DEC-2000; 2000US-025186P.
06-DEC-2000; 2000US-025186P.
06-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P. 05-JAN-2001; 2001US-0259678P 

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM,

WPI; 2001-465460/50. P-PSDB; AAU17136.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

Claim 1; SEQ ID NO 88; 880pp; English.

The invention relates to novel isolated polypeptides (1), and

C polynucleotides (II). (II) and the antibody to (I) are useful for

C polynucleotides (II). (II) and the antibody to (I) are useful for

C diagnosing, preventing and treating diseases including immune system

C disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ

C transplant rejections and graft versus host disease, infectious diseases

CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and

C other blood-related disorders (sickle cell anaemia), myeloproliferative

C disorders, primary haematopoletic disorders, hyperproliferative disorders

C daucher's disease, Parkinson's disease), chromosomal abnormalities

CC Alzheimer's disease, Parkinson's Gisease), chromosomal abnormalities

CC Alzheimer's disease, parkinson's disease), chromosomal disorders (e.g. arrhythmia),

C respiratory disorders, dermatological disorders (e.g. Ardison's

C golumentory disorders, dermatological disorders (e.g. Addison's

C disease), reproductive system disorders (cirrhosis), as stimulators of

C inflammatory disorders, liver disorders (cirrhosis), as stimulators of

C higher affinity antibodies, and as a means to induce tumour pathologies e.g. acquired immune deficiency syndrome (AIDS). AASZ6976
C AASZ7850 represent novel signal transduction pathway protein coding

2021 212 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 8.95e-118 1105.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: Pred. No.: Score:

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Rosen CA,
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(RUBE/) 1
(BARA/) 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilla; thrombocytopenia; immunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction;
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                                                           41 IleGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgileGln
                                                                                                   201 Arccordrigactriaagarcaagaccaragagoragaccocarcaaagrocogaracag
                                                                                                                 | IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrIvsGlnTyrTyrArgArg
                                                                                                                                     ATCTGGGACACTGCAGGGCAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGG
                                                                                                                                                    AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet
                                                                                                                                                                                       LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
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                 MetalalysGlnTyrAspValleuPheArgleuLeuLeuIleGlyAspSerGlyValGly
                          LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   increased serum immunoglobulin concentration
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 US-09-817-198C-2 (1-212) x AAS27053 (1-2021)
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2000US-0180628P.
2000US-0214886P.
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04-FEB-2000; 2
28-JUN-2000; 2
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## 11-702.2009; JOUGNE-0217456P.
## 11-702.2009; JOUGNE-0217456P.
## 11-702.2000; JOUGNE-0217456P.
## 11-702.2000; JOUGNE-0217456P.
## 11-702.2000; JOUGNE-0217456P.
## 4-702.2000; JOUGNE-022256P.
## 4-702.2000; JOUGNE-022256P.
## 4-702.2000; JOUGNE-0222576P.
## 6-702.2000; JOUGNE-0222576P.
## 7-702.2000; JOUGNE-0225576P.
## 7-702.7000; JOUGNE-0225
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acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosting a pathological condition or a susceptibility to presence or absence of a mutation in The nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition based on the presence or absence of the mutation. The polypeptide, the nucleic acid and an antibody to the polypeptide are useful for treating autoimmune disease, Parkinson's disease, silicosis, gastrointestinal disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide, the nucleic acid and the antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. The sequence data for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at sequence uspto.gov/sequence.thml?DocID=20020168711. 

Sequence 2021 BP; 464 A; 564 C; 553 G; 440 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 8.95e-118 1105.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

US-09-817-198C-2 (1-212) x ADB93231 (1-2021)

200 320 260 81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100 40 9 80 141 AAGACCTGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC 41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAG 61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg ATCTGGGACACTGCAGGCAGGAGAAACCAGACCATCACAAAGCAGTACTATCGGCGG 21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 261 8 ద 8 유 8 용 8 셤 ઠે 셤

381 AAGTGGGTCAGTGACGTGGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGG

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501 AAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAG 560 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysPro 200 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnlleLysGlu 141 161 181

> 요. 장 셤

620

180

GluGlyProAlaAsnSerSerLysThrCysTrpCys 212 201

CGGATGCGTGCCAGCAATGAGTTGGCACTGGCAGAGCTGGAGAGGAGGAGGAGGAAACCC 680

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681 GAGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGC 716

AAD47168 

RESULT

AAD47168 standard; cDNA; 3257 BP

AAD47168;

(first entry) 24-FEB-2003 Human Ras-like protein encoding cDNA.

immunodeficiency; procure; protective; Alzheimer's disease; cirrhosis; Parkinson's disease; wasting disease; cachexia; myocardial infarction; parkinson's disease; wasting disease; cachexia; myocardial infarction; osteoporosis; atherosofisons; glomerulonephritis; Crohn's disease; irritable bowel syndrome; multiple solerosis; osteoarthritis; allergy; pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic; Siogren's syndrome; infection; transgenic; gene therapy; nootropic; gout; neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic; ophthalmological; tranquilliser; cancer; stroke; Grave's disease; AIDS; asthma; anaemia; drug screening; gene; ss. Human; Ras-like protein; inflammation; cell proliferation;

Homo sapiens

"Human Ras-like protein" Location/Qualifiers 1. .44 /*tag= a 45. .683 /*tag= b /product= ' Key 5'UTR CDS

584. .3257

3'UTR

/*tag= c

WO200277193-A2

03-OCT-2002.

27-MAR-2002; 2002WO-US009328.

27-MAR-2001; 2001US-00817198.

(PEKE ) PE CORP

Ye J, Di Francesco V, Beasley EM; Gan W,

WPI; 2003-018913/01 P-PSDB; AAE29096. New isolated human Ras-like protein polypeptide, useful for diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma or stroke.

Claim 4; Page 73-74; 82pp; English.

440

The invention relates to human Ras-like protein and its corresponding nucleic acid. The Ras-like protein and DNA is useful in the development of human therapeutics and diagnostic compositions. They are useful in the diagnosis, prevention and treatment of inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS and other infectious or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheinmer's disease, Parkinson's disease, wasting disease e.g. cachaxia, ischaemic injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or cirrhosis, osteoporosis or ancer. They are also used to treat disorders associated with inflammation including allergies, atopic dermatitis, atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus, Grave's disease, glomerulonephritis, gout, irritable bowel syndrome, untoinmune thyroiditis, rheumatoid arthritis, sjogren's syndrome, autoimmune thyroiditis, rheumatoid arthritis, sjogren's syndrome, uveitis, trauma, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections. The antibodies of the invention are useful in

us-09-817-198c-2.rng

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180
pharmacogenomic analysis or for tissue typing. The transgenic animals are useful for studying the function of a Ras-like protein, and identifying and evaluating modulators of its activity. Ras-like protein is used in drug screening assays and its DNA is used in gene therapy. The present sequence is human Ras-like protein encoding cDNA
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                                                                                              Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF1368 polynucleotide sequence SEQ ID NO:2735.
                                                                                              Sequence 3257 BP; 793 A; 892 C; 870 G; 702 T; 0 U; 0
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                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
ce which represent the human ORFX open reading frames 1 to 3161. The ORFX
antiposniatic; antiparkinsonian; nootropic; hepatotropic; vulnerary;
antiposniatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
anticonvulsant; antiarthriti; immunosuppressant; immunostimulant;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
dermatological; immunosuppressive; antiinflammatory; antibacterial;
antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
sequences can be used for determining the presence of or predisposition
to, or preventing or treating pathological conditions associated with an
CORPX-associated disorder. The mucleic acids can be used to express ORPX
crosed to treat cancers; proliferative disorders, neurodegenerative
closed to treat cancers; proliferative disorders, neurodegenerative
closed to treat cancers; proliferative disorders, cardiovascular disease,
cliabetes mellitus, hypertension, hypothyroidism, cholesterol ester
storage, systemic lupus erythematosus, severe combined immunodeficiency
(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
contribage damage, noctural hemoglobinizia, antiinflammatory disease; to vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostipus dermalological; immunosuppressare; antidiabetic; hypotensive; dermatological; immunosuppressave; antidiabetic; antidiabetic; antianaemic; gene therapy; cancer; proliferative disorder; hypotension; antianaemic; gene therapy; cancer; proliferative disorder; hypotension; neurodegenerative disorder; proliferative disorder; proliferative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholseterol ester storage; systemic lupus erythematosus; infection; severe combined immunoeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation; × enhance coagulation; to inhibit thrombosis; and as a contraceptive 461 G; 341 T; 0 U; 2 Other; Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease. 1666 212 0 0 0 6 Matches: Conservative: Mismatches: Indels: Length: 5; Page 1978-1979; 5507pp; English. Sequence 1666 BP; 333 A; 529 C; thrombosis; contraceptive; ss 2.21e-116 1092.00 97.25% 97.25% 98.82% 31-MAR-1999; 99US-0127607B. 02-APR-1999; 99US-0127636B. 05-APR-1999; 99US-0127728P. 30-MAR-2000; 2000US-00540763. 31-MAR-2000; 2000WO-US008621 Leach M; (CURA-) CURAGEN CORP WPI; 2000-602362/57. Percent Similarity: Best Local Similarity: P-PSDB; AAB41604 WO200058473-A2 Shimkets RA, Homo sapiens Alignment Scores: Pred. No.: 05-OCT-2000 Query Match: Score: 

US-09-817-198C-2 (1-212) x AAC75813 (1-1666)

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2000US-0228924P
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31-JAN-2000;

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24-FBB-2000;

16-MAR-2000;

17-MAR-2000;

11-MAR-2000;

19-MAY-2000;

07-JUN-2000;
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07-JUL-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 CCTTCTCTTCAGCTGGCGAAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACC 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCICDACATTAAAGAGICATTACACGCGICIGACAGAGCIGGIGCIGCAGGCCCATAGG 630
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                                                                                                                                               IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArg1leGln
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune WPI; 2001-465460/50. P-PSDB; AAU17555.

The invention relates to novel isolated polypeptides (I), and the antibody to (I) are useful for diagnostiay, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital and acquired immunodeficiencies, autoimmune configurations and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, myeloproliferative diseases, chimary haematopoletic disorders, hyperproliferative disorders (e.g. Gaucher's disease, Parkinson's disease), chromosomal abnormalities (c.g. Gaucher's disease, Parkinson's disease), chromosomal abnormalities (Dom syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. arrythmia), respiratory disorders, dermatological disorders (e.g. arrythmia), respiratory disorders, dermatological disorders (e.g. Addison's epithelial cell proliferation, endocrine disorders (e.g. Addison's chisease), reproductive system disorders (cirrhosis), as stimulators of lingammatory disorders), liver disorders (cirrhosis), as stimulators of thigher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS), AAS26976-Sequences and PCR primers of the invention pathway protein coding Claim 1; SEQ ID NO 507; 880pp; English. disorders and neuronal disorders.

Alignment Scores:	6.910-87	Length:	266
	832.00	Matches:	160
Percent Similarity:	97.56%	Conservative:	0
Best Local Similarity:		Mismatches:	4
Query Match:	75.29%	Indels:	0
DB:	4	Gaps:	0

US-09-817-198C-2 (1-212) x AAS27472 (1-566)

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71	AFGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGGATCCGGGGTGGGCC 130	00
21	LysThrCysLeuLeuCoysArgPhsThrAspAsnGluPheHisSerSerHisIleSerThr 40	_
131	AGACCTGCCTGCTGCGCTTCACCGACAACGAGTTCCACTCGCTCG	0
41	lleGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgileGln 60	_
191	ATCGCTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAG 250	0
61	IleTrpAspThrAlaGlyGluGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 80	
251	ATCTGGGACACTGCAGGCAGGAGAGATACCAGACCATCACAAAGCAGTATCTGCGCGG 310	2
81	AlaGlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100	0
311	GCCCAGGGGATATTTTTGGTCTATGACATTAGCAGCGCGCGC	2
101	LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120	02
371	AAGTGGGTCAGTGACGTGGATGAGGTACCCAGAAGGCGTCCAGAASATCCTTATTGGG 430	90
121	AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140	0
431	ANTANGGCTGATGAGGAGAWACGGCAGGTGGGAAGAGAGCAAGGGCAGCANCTGGCG 490	90
141	LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 16	160
491	AANGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTNAACATTAAAGAG 550	9
161	SerPheThrArg 164	
551	TCATTCACGCGT 562	

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71 ATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGC 130
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08-DEC-2000; 2000US-0251868P.
                           (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                      ss; gene; human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; immunosuppressive agent; adjuvant, enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration.
                                                                                      Human cDNA encoding a novel protein #497.
                           ADB93650 standard; cDNA; 566 BP.
                                                                                                                                                                                                                                                                       2000US-0216647P

2000US-0216880P

2000US-0211487P

2000US-0219290P

2000US-0220964P

2000US-0224519P

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                                                                 04-DEC-2003 (first entry)
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                                              ADB93650;
                   ADB93650
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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide is also useful for identifying a binding patrner to the polypeptide is also useful for identifying a binding patrner and determining whether the binding patrner effects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing the polypeptide or the nucleic acid encoding the polypeptide. The polypeptide or the nucleic acid condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility and useful acid and the antibody to the polypeptide are useful for induce induce immune responses, and as agents to induce data for this patent did not form part of the polypeptides and increase serum immunosuppressive agents from USPTO at pathological condition or susceptibility to the polypeptide or specificat
                                                                                                                                                                                                                                                                                                                        New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; SEQ ID NO 507; 345pp; English.
      Barash SC;
Rosen CA, Ruben SM,
                                                                                                                                 WPI; 2003-719985/68
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Length: Matches: Conservative: Mismatches:

6.91e-87 832.00 97.56% 97.56% 75.29%

Indels:

Conservative: Mismatches:

546.50 72.04% 49.76% 49.46%

Indels:

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ATCTGGGACACTGCAGGGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6176-ABI30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu
                                                                                                                                                               491 AANGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCTAACCTINAACATTAAAGAG
                                                                                                           121 AsniysAlaAspGluGluGluGlnIysArgGlnValGlyArgGluGlnGlyGlnLeuAla
                                                                                                                                AATAAGGCTGATGAGGAGCAGAWACGGCAGGTGGGAAGAGAGCAAGGGCAGCANCTGGCG
                                    AlaGlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet
                                                                LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                                                                                                                                                                                                                                                                                                                                   developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                pharmaceutical; gene; ds
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Sequence 1540 BP; 437 A; 353 C; 420 G; 330 T; 0 U; 0 Other;

from WIPO at ftp.wipo.int/pub/published_pct_sequences

1540

Length:

Alignment Scores: Pred. No.:

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Human, cytokine; cell proliferation; cell differentiation, growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; ofemotexis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; carcer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; issue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiathmatic; antiarthritic; haemostatic; antiarteriosclerotic;
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Gaps:

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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10981-ABB12330 represent nucleic caids encoding them. The invention also relates to vectors and recombinant host calls comprising a nucleotide of the invention, methods of detecting the nucleotides or antibodes against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of detecting the nucleotides or polypeptides for the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence collypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence contains activities, including cytokine, cell proliferation or cell financed activities, activity; have various activities; stem cell growth factor activity; have various activities; activities, membroodiatory activity; tissue growth activity; have various activities, activities, probable biological activities, or may be mematopolesis regulatory activity; tissue growth activities; cremanded activities; chemocatic or chemokinetic activities; polypeptides of morpored activities, activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, hammacoy conditions (e.g., polypeptides and nucleotides of proliferative retinopathy atherosclerosis, coronary heart disease, arterial ischaemia, bone disacrders (e.g., mayeloid or lymphoid cell cuscular growth. Polypeptides involved with tissue regeneration and repair of nucleic acids encoding them) may be used to promote wound repair growth. Polypeptides involved with tissue regeneration and repair of fungal infections in addition to immune disease or activity may be used to promote cell growth. For example, such polypeptides may be used to augment or replace cells deneced or activity may be used to succerning techniques. The disease or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
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                    antifungal; vulnerary; antiulcer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 805; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                 Liu C, Drmanac RT;
                                                                                                                                                                                                                                     03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                                                                                           05-FEB-2001; 2001WO-US003800
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-457740/49.
                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABB11916
                                                                                                       40200157188-A2
                                                                 Homo sapiens
                                                                                                                                                  09-AUG-2001
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07-JUN-2001; 2001WO-US018569.
Homo sapiens
                                      03-JAN-2002.
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99
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43
                            Length:
Matches:
Conservative:
Mismatches:
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                          6.95e-53
545.00
77.01%
52.94%
49.32%
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Query Match:
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Alignment Scores:

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199 ATATGGGACACAGCGGTCAGGAACGGTTTCGGACGATCACAACGGCCTACTACAGGGGT 258
                                                                                                                                                                                                                                                    AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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                                                                                                                                                                                                                                                                                                                                                                                                                      141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                    161 SerPheThrArgieuThrGluLeuValLeuGlnAlaHisArgiysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostetic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 40
                                                                                                                                       IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArglleGln
                                                                                                                                                                                              61 ileTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                          Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ovarian antigen HCGMA67 cDNA, SEQ ID NO:290.
US-09-817-198C-2 (1-212) x ABA09160 (1-1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ArgMetArgAlaSerAsnGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 AGCCCCCAGGGGAGCAACCAG 579
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82 GlnGlyllePheLeuValTyrAspileSerSerGluArgSerTyrGlnHisIleMetLys 101

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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polybrucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens and the use of recombinant vectors and host cells comprising human ovarian antigens and the use of vorarian antigens, and the use of ovarian antigens and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Succonditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system of isorders of ovarian or breast origin, reproductive system of isorders (e.g., infertility, disorders of pregnancy, anovulation.)

CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vagnitis), immune disorders (e.g., cangenital and acquired conditions in disorders (e.g., anaemia), cardiovascular disorders (c.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (c.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (c.g., anaemia), cardiovascu
                                                                                                                                                                                                                                                                                       useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                             Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2411 BP; 600 A; 671 C; 583 G; 547 T; 0 U; 10 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 290; 2922pp; English.
07-JUN-2000; 2000US-0209467P
                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                  Rosen CA;
                                                                                                                                                                       WPI; 2002-147878/19.
P-PSDB; ABP41333.
                                                                                                               Birse CE,
                                                                                                                                                                                                                                                                                                                                                     diseases.
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TGGGACACACAGCGGTCAGGAACGGTTTCGGACGATCACAACGGCCTACTACTACAGGGGTGCA 286 ACCIGIGECCIGITCCGCTICTCCCAGGACGCCTICAACTCCACTITIAICTCCACCAIA 166 GCGAAGACCTACGATTACCTGTTCAAGCTGCTGCTCGATCGGGGACTCGGGGGTGGGGAAG 106 21 ThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIle 41 61 81 2 AlaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLys TrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAla GlyvalAspPheLysMetLysThrlleGluvalAspGlyIleLysValArglleGlnIle 98 7 4 5 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-817-198C-2 (1-212) x ABQ54410 (1-2411) 3.44e-52 540.00 76.88% 52.69% Percent Similarity: Best Local Similarity: Alignment Scores: 42 62 227 Query Match:

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Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and immunomodulatory; muscular active general; vulnerary; gastrointestinal activity in ephrotropic; antiinfective; gynecological, or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardioactive; immunomodulatory; muscular active; vulnerary; asstrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural antibacterial; diagnosis; neural proliferative disorder; wound halling; infectious disease; ds.
287 ATGGGCATCATGCTGGTCTACGACATCACCAACGAGAAGTCCTTCGACAACATCCGGAAC 346
                                                                                406
                                                                                                                                                                                            161
                                                                                                                                                                                                                                                                                   407 AAGTGTGATGTGAATGACAAGACAAGTTTCCAAGGAACGGGGAGAAAAGCTGGCCCTC 466
                                                                                                                         122 LysalaaspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLys 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                                                    467 GACTATGGAATCAAGTTCATGGAGACCAGCGGAAGGCCAACATCAATGTGGAAAATGGA
                                                                                                                                                                                                                                                                 162 PheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArg
                                                                                                                                                                                              142 GluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSer
                                                102 TrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; lung cancer associated protein; neuroprotective; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lung cancer associated polynucleotide sequence SEQ ID 91.
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                                                                                                                                                                                                                                                                                                                                         182 MetArgAlaSerAsnGlu 187
                                                                                                                                                                                                                                                                                                                                                                         587 CCCCAGGGGAGCAACCAG 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF18072 standard; DNA; 1274
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         identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neutal, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein sequences
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sequences may be used for detection of lung cancer, chromosome
                                                                                                         Sequence 1274 BP; 416 A; 267 C; 353 G; 235 T; 0 U; 3 Other;
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AAA40104 standard; cDNA; 716 BP

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This invention describes a novel human Rablo cDNA sequence. The protein coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rablo. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polymucleotide and said polypeptide. This sequence encodes the human Rablo protein described in the method of the invention
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                                                                             Human; Rablo; Yap/Rab family; ss
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215 ACCATAGGAATAGACTTCAAGATCAAAACAGTTGAATTACAAGGAAAGAAGATCAAGCTA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                   275 CAGATATGGGATACAGCAGGCCAGGAGCGATTTCACACCATCACAACCTCCTACTACAGA
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                                                                                                           140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys
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  GlyasnLysalaaspGluGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu
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                                                                                                           ACCATAGGAATAGATTTTAAGATCAAAACAGTTGAATTACAAGGAAAGAAGATCAAGCTA
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                                         GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerBisIleSer
                                                                                193 GGGAAGACCTGCGTCCTTTTTCGTTTTTCGGATGATGCCTTCAATACCACCTTTATTTCC
                                                                                                 ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgile
                                                                                                                                  GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrArg
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                                                                                                                                                                                                  100 MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle
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                                                                                                                                                                                                                                                                                                                                                                                                                       protein; GTPase; GTP binding; gene therapy; cancer;
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Gaps:
               US-09-817-198C-2 (1-212) x AAA40109 (1-888)
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127. .729
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/product= "RAB10"
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                                                                                                                                                                                                                                                                                                                                                     AAA96887 standard; DNA; 956
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P-PSDB; AAB19165.
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AGCAAATGGCTTAGAAACATAGATGCATGCCCAATGAAGATGTGGAAAGAATGTTACTA 486
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                                                                                                                                                                        The present sequence encodes a mammalian RAB protein. RAB proteins constitute the largest family of small GTPases, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes, in producing compositions that modulate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physiological pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression. The DNA may also be used to identify expression of the gene in a biological specimen
   Novel isolated nucleic acid encoding a mammalian RAB protein useful for identifying homologous or related genes, in producing composition that modulates expression or function of RAB for cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle
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Matches:
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Job time : 362 secs
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MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastESE for Windows Version 2.0 CURREY APPLICATION NUMBER: US/08/916,901
FILING APPLICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER:
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NAME: Billings, Lucy J.
RGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08916901
Patent No. 5892012
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
TILE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
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ADDRESSEE: Incyte Pharma
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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-DB=ISBUG_ PatenTe NA -OFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MAR=100 -THR MIN=0 -ALIGN=15
-MODE=LCGAL -OUTPMT=pcc -NORM=ext -HEAPSIZE=500 -MINLENE® -MAXLENE=200000000
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-NO MMAP -LARGEQUERY -NGG_SCORES=0 -MAXIT -DESPENCK=100 -LONGING
-DBT TIMEOUT=120 -WARN TIMEOUT=30 -THERADS=1 .XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 1, Appli
Sequence 16, Appl
Sequence 17, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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   (without alignments)
   1417.465 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC 212
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                         nucleic search, using frame_plus_p2n model
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US-09-154-602-4
US-09-300-958A-16
US-09-016-434-1422
US-09-566-921-7
US-09-620-312D-646
US-09-18-184-2
US-09-075-454-10
US-09-620-312D-959
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No. Result

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Query Match:
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426 AACAAGAGCGACCTCACCACCAGAAGGTGGTGGACAACAACAACAAGGAGTTTGCA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 GACTCTCTGGGCATCCCCTTCTTGGAGACGCGCCAAGAATGCCACCAATGTCGAGCAG 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                          ength:
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Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
                                                                                                                                                            6.68e-52
478.50
65.84%
45.05%
            SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
INFORMATION FOR SEQ ID NO:
                                                                                                LIBRARY: LIVRTUT04
CLONE: 2514506
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                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                         Alignment Scores:
Pred. No.:
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DB:
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101 LygTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLygIleLeuIleGly 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 AIGAACCCCGAATATGACTACCTGTTTAAGCTGCTTTTGATTGGCGACTCAGGCGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
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Matches:
Conservative:
Mismatches:
Indels:
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OPERATING SYSTEM: DOS
SOFTWARE: FRACEG for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-817-198C-2 (1-212) x US-09-154-602-4 (1-925)
                TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
ADDRESSONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
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65.84%
45.05%
43.30%
                                                                         ADDRESSEE: Incyte Pharm
STREET: 3174 Porter Dr
CITY: Palo Alto
                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIVRTUT04
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                                                                                                                                                            USA
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141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                                                                                                                                        81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                         121 AsnLysAlaAspGluGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                    439 ANTANGANTGACGACCCTGAGCGGAAGGTGGTGGAGGACGGAAGATGCCTACAAATTCGCC 498
                                                                                                                                                                                                                                                                                                                               161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                              101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER FEDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEAD FORMS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1422, Application US/09016434

Patent No. 6500308

GENERAL INFORMATION:
APPLICANT: Jeffrey J. Seilhamer
ITILE OF INVENTION: COMPOSITION FOR THE DETECT
ITILE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION:
(650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ArgMetArgAlaSerAsnGluLeu 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1422:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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US-09-016-434-1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-016-434-1422
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APPLICANT: MCCLelland, Michael
APPLICANT: Tenkke, Thomas
FAPLICANT: Trank, Thomas
TITLE OF INVENTION: Using Same
TITLE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR APPLICATION NUMBER: 60/089,070
FRIOR APPLICATION NUMBER: 60/098,070
FRIOR APPLICATION NUMBER: 60/18,624
FRIOR APPLICATION NUMBER: 60/118,624
FRIOR APPLICATION NUMBER: 60/118,624
FRIOR PILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
121 AsniyaAlaAspGluGluGlniyaArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                                                                                            591 GGAGCAGCCTCTGGGGGGGGGGCGCCCAATCTCAAGATGGACAGCACCCCTGTAAAGGCGG 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 ATGGCCCGGGACTACGACCTCTTCAAGCTGCTCATCATCGGCGACAGCGGTGTGGGC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 ATCGGAGTGGATTTCAAGATCCGGACCGTGGAGATCAACGGGGGAGAGGTGAAGCTGCAG 261
                                    426 AACAAGAGCGACCTCACCACCAAGAAGGTGGTGGACAACACCCACGAGGAGTTTGCA 485
                                                                              141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                             161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                                              181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysPro 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IleTrpAspThrAlaGlyGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 80
                                                                                                        ----ATGACCATGGCTGCTGAAATCAAAAGCGGATGGGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09300958A
Patent No. 6495319
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477.50
72.34%
46.28%
43.21%
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Best Local Similarity:
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Pred. No.:
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LENGTH: 730
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121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 GATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGAATGTAGAACAG 691
                                                                                                                                                                                                                                       41 ileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgIleGln 60
                                                                                                                                       212 ATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCAGGGGTTGGA
                                                                                                                                                                                                                                                        332 ATTGGTGTGGATTTCAAAATAAGAACTATAGAGTTAGAGGGAAAACAATCAAGCTTCAA
                                                                                                                                                                                                                                                                                                61 ileTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
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                                                                                                                    1 MetalaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids
TITLE OF INVENTION: Polypeptides
                                                                                         US-09-817-198C-2 (1-212) x US-09-566-921-7 (1-8137
   Matches:
                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REPERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 646, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Xang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Wang, Zhiwei
John Tillinghast
 467.00
72.84%
51.85%
42.26%
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                Similarity:
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               Percent Simil
Best Local Sin
Query Match:
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                                                                                                                                                                 60 Argaarcccgaararcarrrrrrrrrrrrarccaarrrcccaarrcccaacrcaccccaarrcca
                                                                                                                                                                                            LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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                                                                                                                                                                                                                                                                                                                                                                          81 AlaGlnGlyilePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09566921

Patent No. 6682888

GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION UNDERS: US/09/566,921

CURRENT FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 138

SOFTWARE: PERL PROGram

SEQ ID NO 7

LENGTH: 8137
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OTHER INFORMATION: Incyte ID No. 6682888 411474.10
NAME/KEY: ungure
LOCATION: 3468-3788
OTHER INFORMATION: a, t, c, g, or other
                Matches:
Conservative:
Mismatches:
Indels:
                                                                                                      US-09-817-198C-2 (1-212) x US-09-016-434-1422 (1-723)
    Length:
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                             Percent Similarity:
Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 TCAACTCAAATCAAAACATACTCTTGGGACAATGCCCAAGTTATTCTGGTTGGGAACAAG 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 AlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGlu 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 ThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMet 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysProGluGly 202
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                                                                                                                                                                                                                                                                                                                                                                              228 cagaactitigactacatgricaaattactcatcatcgcaatagcagtggggaaaaaaa 287
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83
49
71
                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                     US-09-817-198C-2 (1-212) x US-09-620-312D-646 (1-1069)
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PRIOR APPLICATION NUMBER: 09/488,725
           PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: Pt_FL_genes Version 1.0
SEQ ID NO 646
LENGTH: 1069
                                                                                                                                                                                                            5.54e-49
456.50
62.86%
39.52%
41.31%
                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (156)..(839)
US-09-620-312D-646
                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                              Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 TACGACGTCGCCTTCAAGGTCATGCTGGGGGGGACTCGGGTGTGGGGAAGACCTGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 laspphelysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAs
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
COTWARRE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,873
FILING DATE: Filed Herewith
CLASSIFICATION: 435
... rulCANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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Matches:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TREECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1340 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437.50
67.84%
45.23%
39.59%
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                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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260

Sequence 2, Application US/08824873 Patent No. 584317 GENERL INFORMATION: APPLICANT: Hillman, Jennifer L.

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321 GACCGAGATCCACGAGAGGCGCAGGAGGAGGGGGCTCATGCTGCTGGGGAACAAGGT 380
                                                                                                                                                                                                                                                                                                                                                                                              143 rGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheTh 163
                                                                 ::: ||||::|||||||||:::
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                                                                                                                                                                                                                                                                                                           103 lSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLysAl
22 TACGACGTCGCCTTCAAGGTCATGCTGGTGGGGGACATCTCGGGTGTGGGGGAAGACCTGTCTG
                                                                                                               43 lAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAs
                                                                                                                               prhrAlaGlyGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGl
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,454
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lall, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
APPLICANT: Batra, Sajeev
APPLICANT: Batra, Rajev
TITLE OF INVENTION: Mariah R.
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-075-454-10
; Sequence 10, Application US/09075454
; Patent No. 6391580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: US
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Mismatches:
Indels:
Gaps:
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CSRFTWARE: PESESED for Windows Version 2.0
CNFRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,184
                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09198184

Patent No. 6010859

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Geogler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is Diskette
IBM Compatible
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LENGTH: 1340 base pairs
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67.84%
45.23%
39.59%
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
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SOFTWARE: FASTSEC
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CITY: Palo Alto
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LIBRARY: PANCIL
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INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 GlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 ArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg 183
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-817-198C-2 (1-212) x US-09-075-454-10 (1-875)
            ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMMUNICATION:
TELECHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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US-09-620-312D-959
; Sequence 959, Application US/09620312D
FILING DATE: DECEMBER 12, 1996
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429.00
68.48%
44.57%
38.82%
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INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; CLONE: 1528559
US-09-075-454-10
                                                                                                                                                                                                                   TOPOLOGY: linear IMMEDIATE SOURCE:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                             Alignment Scores:
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103 TACGACCTCACGGGCAAGGTGATGCTTCTGGGAGACACAGGCGTCGGCAAAAACATGTTTC 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 AspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAsp
                                                                                                                                                                                                                                                                                                                APPLICANT: Drmanac, Radoje T.
IIILE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PRILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 959
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Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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68.48%
44.57%
38.82%
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John Tillinghast
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
Wang, Dunrui
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ORGANISM: Homo sapiens
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US-09-620-312D-959
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Best Local Similarity:
Query Match:
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NAME/KEY: CDS
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183
                                                                  144 GlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThr 163
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124 AspGluGluGluLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyr 143
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                    164 ArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg
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83
68
12
12
                                                                                                                                                                             ----GAGTTAGCCTTTCTGGCCATCGCCAAGGAA---
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TITLE OF INVENTION: No. 656966el Nucleic Acids and
TITLE OF INVENTION: No. 656966el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
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Mismatches:
Indels:
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Matches:
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PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEG ID NOS: 1105
SOFTWARE: Pt_genes Version 1.0
SEQ ID NO 426
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60.98%
40.49%
38.37%
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John Tillinghast
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Ren, Feiyan
Chen, Rui-hong
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Wehrman, Tom
Xue, Aidong J.
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
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Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
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ORGANISM: Homo sapiens
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Best Local Similarity:
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, LOCATION: (95)
US-09-620-312D-426
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 GlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThr 163
                                                                                                                                                                    568 -----CAGTTAGCCTTTCTGGCCATCGCCAAGGAA-----CTGAAATACCGG 609
                        164 ArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg 183
   124 AspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyr 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyraspvalleuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLysThrCysLeu
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                                                                                            FEATURE:
NAMENKEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 412477.1CB1
US-09-484-9708-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-817-198C-2 (1-212) x US-09-484-970B-142 (1-2612)
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Matches:
Conservative:
Mismatches:
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APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION UNMERE: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
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Patent No. 6426186
GENERAL INFORMATION:
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429.00
68.48%
44.57%
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610 GCCGGCCATCAG 621
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                JS-09-484-970B-142
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SEQ ID NO 142
LENGTH: 2612
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Pred. No.:
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GluThrSerAlaCygThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGluLeu 168
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Matches:
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63.24%
42.65%
38.37%
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LOCATION: (138)
OTHER INFORMATION:
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OTHER INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                    NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                  125 GluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyrGly 144
                                                                                                                                                                                                                                                                                                                                                                                   145 MetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArg 164
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                                                                                                                                                                                85 PheleuValTyrAspileSerSerGluArgSerTyrGlnHislleMetLysTrpValSer 104
                                                                                                                                                                                                                                                   105 AspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLysAlaAsp 124
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                                                   64
                                                                                                                 65 AlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIle 84
                                                 PhelysMetLysThrileGluValAspGlyIleLysValArgileGlnIleTrpAspThr
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581 ACAGCCAAA-----GAAATATATAGGAAGATCCAGCAGGGTTTA-----
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OTHER INFORMATION: The n at positions 6 through 8 represents an OTHER INFORMATION: unknown.
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APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Lory Ying
APPLICANT: Luo, Ying
APPLICANT: Shen, Mary
TITLE OF INVENTION: Shen, Mary
TITLE OF INVENTION: A65905-1/DUB/RMS
CURRENT APPLICATION NUMBER: US/09/255,920A
CURRENT FILING DATE: 1999-02-23
PRIOR FILING DATE: 1998-02-23
PRIOR PELLING DATE: 1998-02-23
PRIOR APPLICATION NUMBER: 60/086,650
PRIOR FILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: The
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LOCATION: (6)..(
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-09-255-920A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 6
LENGTH: 842
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TyralaProGluGlyValGlnLysIleLeuIleGlyAsnLysAlaAspGluGluGlnLys 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspileSerSerGluArgSerTyrGlnHisIleMetLysTrpValSerAspValAspGlu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLyBGluTyrGlyMetABpPheTyr 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ArgleuleuleulleGlyAspSerGlyValGlyLysThrCysLeuleuCysArgPheThr 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 AspAsnGluPheHisSer---SerHisIleSerThrIleGlyValAspPheLysMetLys 48
                                                                                                                                       LOCATION: (17)..(18)
OTHER INFORMATION: The n at positions 17 through 18 represents an OTHER INFORMATION: unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (204)
. OTHER INFORMATION: The n at position 204 represents an unknown.
US-09-255-920A-6
                                                                        represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (108)
OTHER INFORMATION: The n at position 108 represents an unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The n at position 823 represents an unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The n at position 138 represents an unknown
                                                                                                                                                                                                                                                                                                                                                                                                  The n at position 726 represents an unknown
                                                                                                                                                                                                           NAME/KEY: ungure
LOCATION: (22)
OTHER INFORMATION: The n at position 22 represents an unknown
                                                                                                                                                                                                                                                                                                      LOCATION: (25)
OTHER INFORMATION: The n at position 25 represents an unknown.
OTHER INFORMATION: The n at position 12 represents an unknown
         LOCATION: (14)..(15)
OTHER INFORMATION: The n at positions 14 through 15
NAMEK EXY: unknown.
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Mismatches:
Indels:
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125 GlugluglnLysArgGlnValGlyArgGluGlnGlnGlnGlnLeuAlaLysGluTyrGly 144
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---GluGluGl 196
                                                                                  85 PheLeuValTyrAspileSerSerGluArgSerTyrGlnHisIleMetLysTrpValSer 104
                                                                                                                                                                                                                 105 AspValAspGluTyrAlaProGluGlyValGlnLysIleLeuileGlyAsnLysAlaAsp 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 MetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArg 164
                                                                                                                           165 LeuThrGluLeuVal-LeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg--
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Sequence 28, Application US/08888077A

Sequence 28, Application US/08888077A

Setent No. 6020143

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMENS, JOHANNA M

APPLICANT: RAMSER, PAUL E

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
ADDRESSE: LERRIER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK

STREET: 600 SOUTH AVENUE WEST

CITY: WESTFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIP IV
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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COUNTRY: USA
ZIP: 07090-1497
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                                                                                                                                                                                           189 AlaLeuAlaGluLeuGluGluGluGluGlyLysProGlu-GlyProAlaAsmSerSerLy 208
                                                                                                                                                                                                                              |||:: ||||:: |||||:: ||||:: ||||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: ||:: |||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: ||:: ||:: ||:: ||: ||:: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
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      --GAGTTG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 PhelysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAspThr 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 AlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlylle 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyraspvalleuPheArgLeuLeuLeulleGlyaspSerGlyvalGlyLysThrCysLeu 24
                                                                                                                           574 GCCTTTCTGGCAATTGCCAAGGAA-----CTGAAATACCGTGCAGGGAGGCAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: Betry, Maria
APPLICANT: Ling, Huai-Ping
APPLICANT: Ling, Huai-Ping
APPLICANT: An, Wendian
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: MNI-070CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1998-11-30
EARLIER FILING DATE: 1998-11-30
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: USSN 09/298,731
EARLIER FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: USSN 09/350,614
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN VOY: 2.0
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EARLIER APPLICATION NUMBER: USSN 60/110,277
      538 GAGACCAGTGCCAAGACTGGCATGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 66, Application US/09399913 Patent No. 6361971
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64.59%
40.67%
37.92%
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ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1)
US-09-399-913-66
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124 AspGluGluGluLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyr 143
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                                                                                                                                                                                                                                                                                                                                                 312 GCCTTATTGGTTTATGACATTGCTAAACATCTCACATATGAAAATGTAGAGCGATGGCTG 371
                                                                                                                                                                                                                                                                                                                                                                                                                              GlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPhe--- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 ThrargleuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArg--- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----MetArgAlaSerAsnGluLeuAlaLeuAlaGluLeu---GluGluGluGluGly 198
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                                                                                                                                                                                                                                                        44 AspPheLysMetLysThrileGluvalAspGlyIleLysValArgIleGlnIleTrpAsp 63
                                                                                                                                                                                                                                                                                             64 ThralaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGly
                                                                                                                                                                                                              24 LeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIleGlyVal
                                                                                970
85
45
68
3
                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...970
; OTHER INFORMATION: /note= "Y2H9"
                                                                              2.87e-43
411.50
64.04%
41.87%
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                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                      Alignment Scores:
Pred. No.:
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Title: Perfect score:

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Sequence 507, App
Sequence 256, App
Sequence 21, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 39, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 884, App
Sequence 884, App
Sequence 884, App
Sequence 2241, App
Sequence 236, App
Sequence 16115, App
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Sequence 2336, App
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Sequence 23151, App
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Sequence 5, Appli
Sequence 5, Appli
Sequence 529, Appl
Sequence 529, App
Sequence 43925, A
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Sequence 241, App
Sequence 4, Appli
Sequence 48, Appl
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Sequence 17495, A
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERBROE: 21272-113 (793)
FILE REPERBROE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 74
LENGTH: 1054
12 US-10-363-616-74 MPA
9 US-09-764-868-88 ABA
9 US-09-817-198A-1
9 US-09-1817-198A-1
15 US-10-184-817-256
14 US-10-084-817-256
19 US-09-925-300-631
19 US-09-925-300-631
19 US-09-925-300-631
19 US-09-194-257-7
9 US-09-794-257-7
9 US-09-834-975-895
9 US-09-834-975-895
9 US-09-834-975-896
14 US-10-128-714-7241
14 US-10-128-714-7600
9 US-09-938-822A-836
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US-10-425-114-16115

US-10-425-114-12044

US-10-425-114-12044

US-10-425-114-12044

US-10-425-114-12044

US-10-425-114-25934

US-10-425-114-2438

US-10-425-114-3413

US-10-425-114-3413

US-10-425-114-3413

US-10-425-114-3414

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US-10-425-114-3414

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US-10-221-278-5

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US-09-770-445-529
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; Sequence 74, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1054)
OTHER INFORMATION: n = a,t,c or
    1898
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ORGANISM: Homo sapiens
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-LOGPC_forz 1/USPTO spool p/USO9817198/runat_15032004_101745_20492/app_query.fasta_1.391
-DS=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITG=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pcto -NORM=ext -HEARBIZE=500 -MINLEN=0
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pcto -NORM=ext -HEARBIZE=500 -MINLEN=0
-TRANS=NORM - NORM -LARGEQUERY -NEG SCORE=s0 - WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMBOTT=120 -WARN TIMBOTT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                               March 21, 2004, 08:59:39; Search time 311 Seconds (without alignments) 2521.609 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                          1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC 212
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1. (cgn2_6/ptodata/2/pubpna/DSO7 PUBCOMB.seq:*
2. (cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3. (cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4. (cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5. (cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6. (cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
7. (cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
8. (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9. (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
13. (cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
14. (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
15. (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
16. (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
17. (cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
18. (cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
19. (cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
11. (cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
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17. (cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                      OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext '
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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                      Length:
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ORGANISM: Homo sapiens
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Patent No. US20020146758A1
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: NUMBER: US/09/817,198A
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 1.
LENGTH: 3257
                                                                                                                                                                                                                         101 ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGAGGTAGACGGCATCAAAGTGCGGATACAG
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Length:
Matches:
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Mismatches:
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Sequence 507, Application US/09764868
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32 - 1723 - 1721.
FILE REFERENCE: PTZ32 - 2001-01-17
CURRENT FILING DATE: 2001-01-17
FILE PLANDER: OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: DAA
TYPE: DNA
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Matches:
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Best Local Similarity:
Query Match:
DB:
; ORGANISM: Human
US-09-817-198A-1
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Publication No. US2004005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PA13791
CURRENT APPLICATION WMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
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                                             LOCATION: (493)
OTHER INFORMATION: IN NAME/KEY: SITE
LOCATION: (538)
OTHER INFORMATION: IN NAME/KEY: SITE
LOCATION: (563)
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Best Local Similarity:
Query Match:
DB:
LOCATION: (484)
OTHER INFORMATION:
NAME/KEY: SITE
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US-09-764-868-507
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LysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLys 141
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OTHER INFORMATION: Incyte ID No. US20030119009A1 4004223CB1
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APPLICANT: Jed G. Nuchtern
APPLICANT: Sharon B. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-25
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Publication No. US20030119009A1
GENERAL INFORMATION:
APPLICANT: Susan Stuart
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PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL Program
SEQ ID NO 256
LENGTH: 995
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ORGANISM: Homo sapiens
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LOCATION: (2309)...(2309)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (2357)...(2357)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (21)...(21)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (17)..(17)
OTHER INFORMATION: n equals a,t,g,
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PRIOR FILING DATE: 2001-00-00, PRIOR APPLICATION NUMBER: US 60/07 NUMBER OF SEQ ID NOS: 4360 SOFTWARE: Patentin Ver. 3.1 SEQ ID NO 290 LENGTH: 2411
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
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Best Local Similarity:
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parent No. US2020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT APPLICATION NUMBER: DCT/US00/05988

PRIOR APPLICATION NUMBER: PCT/US00/05988

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEC ID NO 631

LENGTHAL: 1537
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                                                                   US-09-817-198C-2 (1-212) x US-09-925-302-91 (1-1274)
   Gaps:
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ORGANISM: Homo sapiens
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247 ATCGGAATTGATTTCAAGATCCGCACTGTGGATATAGAGGGGAAGAAGATCAAACTACAA 306
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Fatent No. US20020044941A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
FRIOR PELING DATE: 2000-03-08
FRIOR PILING DATE: 2000-03-08
FRIOR PILING DATE: 1999-03-12
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR PILING DATE: 1999-03-12
NUMBER OF SEC ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
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; OTHER INFORMATION: n equals a,t,g,
US-09-925-302-91
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NAME/KEY: misc feature
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; Sequence 9, Application US/09794257; Patent No. US20020009804A1; GENERAL INFORMATION:
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528.50
80.68%
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                                                    530.50
82.56%
55.81%
48.01%
                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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ORGANISM: homo
                          Alignment Scores:
Pred. No.:
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Pred. No.:
JS-10-096-534-38
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US-10-096-534-38

US-10-096-534-38

Sequence 38, Application US/10096534

Publication No. US20030166887A1

GENERAL INFORMATION:

APPLICANT: The Brigan and Women's Hospital, Inc.

APPLICANT: Wizuno, Shuichi

APPLICANT: Mizuno, Shuichi

APPLICANT: Mizuno, Shuichi

APPLICANT: Mizuno, Shuichi

APPLICANT: Wizuno, 10,244/KA/ERP

CURRENT APPLICATION NUMBER: US 60/274,980

PRIOR APPLICATION NUMBER: US 60/274,980

PRIOR FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.0

SEQ ID NO 38

LENGTH: 3164

TYPE: DNA

CREANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GlyAsnLysAlaAspGluGluGlnIysArgGlnValGlyArgGluGlnGlyGlnGlnLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
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833 AGCADATGGCTTAGAAACATAGATGAGCATGCCAATGAAGAATGTGGAAAGAATGTTACTA 892
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                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                     Gaps:
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                           DOCATION: (5)
CTHER INFORMATION: n equals a,t,g,
US-09-925-300-631
                                                                                             1.75e-57
530.50
82.56%
55.81%
  FEATURE:
NAME/KEY: misc feature
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Best Local Similarity:
Query Match:
                                                                                    Alignment Scores:
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APPLICANT: Meyers. Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804Alel
TITLE OF INVENTION: Human G-Proteins
FILE REPERENCE: 35800/20286
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,606
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                          390
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Length:
Matches:
Conservative:
Mismatches:
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Patent No. US20020009804A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804A1e1
TITLE OF INVENTION: Human G-Proteins
FILE REFERENCE: 35800/209285
CURRENT APPLICATION NUMBER: 60/195,606
PRIOR APPLICATION NUMBER: 60/185,606
PRIOR APPLICATION NUMBER: 60/185,606
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                            81 AlaGlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                                              #21 ATTGACTATGGGATTAAATTCTTGGAGACAAGGGCAAAATCCAGTGCAAATGTAGAAGAG #80
                                                                                                                                           81 ATATGGGACACAGCGGGTCAGGAAAGATTCCGAACAATCACGACAGCGTACTACAGAGGA 240
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                                                                           1 MetAlaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
                                                                                                                          21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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Mismatches:
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                                                  US-09-817-198C-2 (1-212) x US-09-794-257-9 (1-624)
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US-09-794-257-7
  Best Local Similarity:
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Query Match:
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Pred. No.:
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          Query Match:
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APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Boot, Andrew
APPLICANT: Boot, Andrew
APPLICANT: Boot, Andrew
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REPERENCE: MRI-0168
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SSOTWARE: FASTESCQ for Windows Version 4.0
SSQ ID NO 879
LENGTH: 2497
                                                                                                                                                                                                                                                                                                                                                 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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                                      MetAlaLysGlnTyrAspValLeuPheArgLeuLeuIeuIleGlyAspSerGlyValGly
                                                          161 Ser---PheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLys 175
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Matches:
Conservative:
Mismatches:
US-09-817-198C-2 (1-212) x US-09-794-257-7 (1-1161)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 879, Application US/09834975; Patent No. US20020110815A1; GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TILLE REFERENCE: MRI-0168
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER: OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 894
LENGTH: 2497
                                                                                                                                                                                                                                                                                                               81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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Mismatches:
                                                                                                US-09-817-198C-2 (1-212) x US-09-834-975-885 (1-2497)
                                           Indels:
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OTHER INFORMATION: n = A, T, C or
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ORGANISM: Homo sapiens
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| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Lillie, James
| APPLICANT: Bolt, Andrew
| APPLICANT: Bolt, Andrew
| APPLICANT: Wan Huffel, Christophe
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
| TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, OF HUMAN CANCERS
| TITLE OF INVENTION: OF HUMAN CANCERS
| FILE REFERENCE: MRI-0168
| CURRENT APPLICATION NUMBER: US/09/834,975
| CURRENT FILING DATE: 2001-04-13
| PRIOR PILING DATE: 2000-04-14
| NUMBER OF SEQ ID NOS: 1046
| SOFTWARE: FEALESQ for Windows Version 4.0
| SEQ ID NO 885
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Patent No. US20020110815A1
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ORGANISM: Homo sapiens
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Sequence 896, Application US/09834975

Patent No. US20020110815A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Bolt, Andrew

APPLICANT: Bolt, Andrew

APPLICANT: Bolt, Andrew

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APPLICANT: Bolt, Andrew

APPLICANT: Bolt, Andrew

APPLICANT: Wan Huffel, Christophe

TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 15, 2004, 11:12:58; Search time 20 Seconds (without alignments) 1019.630 Million cell updates/sec Run on:

US-09-817-198C-2 Perfect score:

Seguence:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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PIR_78:*
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3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Scor	to	Lengt	DB	Α	Description
	1077	97.5	212	5	F42148	GTP-binding protei
7	559	50.6	224	N	T33855	П
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9	531.5	48.1	200	N	A38625	
7	530.5	48.0	200	~	D36364	
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6	526	47.6		7	178851	
10	522.5	47.3		~	B42148	GTP-binding protei
11	519	47.0		8	T45901	GTPase Atrabs - Ar
12	514	46.5		~	T28971	hypothetical prote
13	512	46.3		7	833900	Ω
14	512	46.3		~	T48378	
15	510	•		~	812790	
16	509	46.1		0	T14565	
17	508.5	46.0		~	S57478	
18	508	46.0		8	JS0640	
13	507.5	4		7	T14405	-1
20	206	45		7	857471	
21	505.5	4		~	836365	
22	502.5	4	215	7	857462	
23	501	4	203	~	S51495	
24	495.5	44.	204	7	JC7589	U
25	492.5	4	215	7	S57474	ď
56	483.5	43	208	~	A34716	
27	483	43.7		7	A38202	
28	482	43.6		~	S34253	
59	480	43.4	202	~	S38740	

hypothetical protein D1037.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Dace: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-Jan-2000 C;Accession: T33858 C;Accession: T33858 R;Ledwith, J.; biewald, T. Submitted to the EMBL Data Library, November 1998 A;Description: The sequence of C. elegans cosmid D1037.

RESULT 2

GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei	ARA-5 [imported] -	GTP-binding protei	GTP-binding protei	hypothetical prote	GTP-binding protei	ras protein homolo	GTP-binding protei			GTP-binding protei
B34716 S72515	JC2488	JC4105	JC5337	S41430	B86153	JC1247	S30096	T33781 ·	T14391	T18242	B38202	TVBYQ4	538339	TVRTYP
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203	201 2	203	201	202	258	203	203	205 2	206	210 2	203	215	205	202
43.3 203 2	•		••	••	.,	•••		•	•	•	•••	•		
	43.2	43.2	43.2	43.2	43.1	43.0	43.0	42.9	42.8	42.8	42.6	42.6	42.4	42.4

## ALIGNMENTS

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A, Molecule type: mRNA
A, Residues: 1-212 <ELEP
A, Cross-references: GB:M93679; NID:g206536; PIDN:AAA41995.1; PID:g206537
A, Cross-references: GB:M83679; NID:g206536; PIDN:AAA41995.1; PID:g206537
C, Superfamily: ras transforming protein; translation elongation factor Tu homology
C, Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine
F;9-124/Domain: translation elongation factor Tu homology <ETU>
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;121-124/Region: GTP-binding NKXD motif
F;210,212/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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GTP-binding protein rab15 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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Best Local Similarity 97.6'
Matches 207; Conservative
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A; Molecule type: mRNA
A; Residues: 1-207 < CHA>
A; Cross-references: GB:X56385; NID:g920; PIDN:CAB56776.1; PID:g6006436
A; Cross-references: GB:X56385; NID:g920; PIDN:CAB56776.1; PID:g6006436
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; F
F; P-124/Domain: translation elongation factor Tu homology < BTU>
F; P-124/Region: GTP-binding motif A (P-loop)
F; P: 121-124/Region: GTP-binding NAX/L motif
F; P: 151-153/Region: GTP-binding SAK/L motif
F; P: 151-154/Region: GTP-binding SAK/L motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Canis lupus familiaris (dog)
C;Accession: 85364; Bsequence_revision 28-Mar-1991 #text_change 02-Feb-2001
C;Accession: 85364; B5564
R;Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A;Title: Molecular cloning of YPTI/6BC4-related CDNAs from an epithelial cell line. A;Reference number: A36364; MUID:91061765; PMID:2123294
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C,Superfamily: ras transforming protein; translation elongation factor Tu homology
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61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                             61 IWDTAGQERFRITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEBHASADVEKMILG 120
                                                                                                                                                              NKADEEÇKRQVGREÇGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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99; Conservative 4
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A;Molecule type: mRNA
A;Residues: 1-203 <ZAH>
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A;Title: A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cell A; Reference number: A49647; MUID:94124602; PMID:8294494
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**Residues: 175-186 <-008.
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**A. Residues: 
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A;Introns: 10/3; 62/2; 82/3; 181/1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
                                                                                                                                                                                                   A;Cross-references: EMBL:AF106592; PIDN:AAC78494.1; GSPDB:GN00119; CESP:D1037.4
A;Experimental source: strain Bristol N2; clone D1037.
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Jan-2001
C;Accession: B49647; S36817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.6%; Score 559; DB 2; Best Local Similarity 55.3%; Pred. No. 2.4e-37; Matches 105; Conservative 42; Mismatches 39
                    A;Accession: T33855
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 EMRAATGAAI 186
    A;Reference number: Z21424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-207 <ZAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                  A; Residues: 1-224 < LED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: CESP:D1037.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
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Best Local S
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A)Cross-references: GB:M38391

G)Superfamily: ras transforming protein; translation elongation factor Tu homology

G;Reywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; I

E;9-124/Domain: translation elongation factor Tu homology «ETU»

F;9-12-124/Region: GTP-binding motif A (P-loop)

F;15-124/Region: GTP-binding MAK/L motif

F;150-152/Region: GTP-binding SAK/L motif

F;206/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-200 < CHA>
A; Residues: 1-200 < CHA>
A; Cross-references: GB: X56387; NID: g914; PIDN: CAA39798.1; PID: g915
A; Cross-references: GB: X56387; NID: g914; PIDN: CAA39798.1; PID: g915
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; F; 10-125/Domain: translation elongation factor Tu homology < ETU>
F; 10-23/Region: nucleotide-binding motif A (P-loop)
F; 122-155/Region: GTP-binding NKXD motif
F; 152-154/Region: GTP-binding SAK/L motif
F; 152-154/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Discopyge ommata
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C;Accession: 188625
A;Fitle: A family of ras-like GFP-binding proteins expressed in electromotor neurons.
A;Reference number: A38625; MUID:91115900; PMID:1899244
A;Status: preliminary
                            Richavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A; Fitle: Molecular cloning of YPTI/SEC4-related cDNAs from an epithelial cell line.
A; Reference number: A36364; MUID:91061765; PMID:2123294
A; Scession: D36364
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQ-YDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             F;199,200/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.0%; Score 530.5; DB 2; 55.8%; Pred. No. 3.8e-35; iive 46; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.0%; Score 530; DB 2;
llarity 47.4%; Pred. No. 4.4e-35;
Conservative 56; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 55.8
Matches 96; Conservative
        C; Accession: D36364; S15601
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99; Conserv
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A; Residues: 1-209 <NGS>
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Matches
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                                                                                                                                            Lys, Asp, Ser) #sta
C; Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; F; 9-124/Domain: translation elongation factor Tu homology <ETU>
F; 15-22/Region: nucleotide-binding motif A (P-loop)
F; 121-124/Region: GTP-binding SXK/L motif
F; 151-153/Region: GTP-binding SAK/L motif
F; 151-22,40,121,122,124,151/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #ste F; 200/Binding site: farnesyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Discopyge ommata
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C;Datession: A38625
R;Ngsee, J.K.; Biferink, L.A.; Scheller, R.H.
J. Biol. Chem. 266, 2675-2680, 1991
A;Title: A family of ras-like GTP-binding proteins expressed in electromotor neurons.
A;Reference number: A38625; MUID:91115900; PMID:1899244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Cross-references: GB:M38390, NID:g213114, PIDN:AAA49230.1; PID:g213115
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F;10-125/Domain: translation elongation factor Tu homology <ETU>
F;16-23/Region: nucleotide-binding motif A (P-loop)
F;12-125/Region: GTP-binding NKXD motif
F;152-154/Region: GTP-binding SAK/L motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKAYDHLFKLLLIGDSGVGKTCLIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKIKLQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKO-YDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D36364
GTP-binding protein rabl0 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                      1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                  18; Gaps
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                                                                                                                                                                                                                            2; Length 203;
                                                                                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        electric ray (Discopyge ommata)
                                                                                                                                                                                                                         48.1%; Score 532; DB 2
47.6%; Pred. No. 3e-35;
rative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRRSGN-----GNKP--PSTDLKTC 192
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                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.65
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-200 <NGS>
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C;Accession: T45901

R;Blocker, H; Mewwes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M. submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aintrons: 25/1; 49/2; 83/1; 105/1; 137/3; 158/3; 189/3
A;Note: F49L2.310
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
F;16-131/Domain: translation elongation factor Tu homology <FTU>
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                                                                                                                                                                                                                                                                                                                                            61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 AGQERFRITTTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDSVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKKTYDLLFKLLLIGDSGVGKTCVLFRPSDDAFNTTFISTIEIDFKIKTVELQGKKIKL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2891
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
R;Wamsley, P.; Bradehaw, H.
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R;Wamsley, P.; Bradehaw, H.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 YDYLIKLLIGDSGVGKSCLLRRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIMDT
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                                                                                                                             1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                   1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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    ; Pred. No. 1.7e-34;
46; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: T45901
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-216 <BLO>
A;Cross-references: EMBL:AL132966
A;Experimental source: cultivar Columbia; BAC clone F4P12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T28971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTPase AtRAB8 - Arabidopsis thaliana
    55.2%;
Best Local Similarity 55.29
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 51.9 Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 TIKINQSDQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 GLRMRASNE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 3
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Accession: B42148
R;Elferink, L.A.; Anzai, K.; Scheller, R.H.
J. Biol. Chem. 267, 5768-5775, 1992
A;Title: rabl5, a novel low molecular weight GTP-binding protein specifically expressed A;Reference number: A42148; MUID:92210533; PMID:1313420
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: ras transforming protein; translation elongation factor Tu homology C; Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine F; 9-124/Domain: translation elongation factor Tu homology <ETU>F; 15-22/Region: nucleotide-binding motif A (P-loop) F; 121-124/Region: GTP-binding MXXD motif F; 151-153/Region: GTP-binding SAK/L motif F; 151-153/Region: GTP-binding CAK/L motif F; 203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: ras transforming protein; translation elongation factor Tu homology C; Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine F;10-125/Domain: translation elongation factor Tu homology <BTU>F;16-21/Region: nucleotide-binding motif A (P-loop)
F;122-125/Region: GTP-binding NKXD motif F;152-154/Region: GTP-binding SAK/L motif F;159,200/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                               GTP-binding protein MEL - mouse

NyAlternate names: gene MEL protein

C,Species: Mus sp. (mouse)

C,Species: Mus 1996 #sequence_revision 02-Aug-1996 #text_change 02-Feb-2001

C,Accession: 178851

R;Nimmo, E.R.; Sanders, P.G.; Padua, R.A.; Hughes, D.; Williamson, R.; Johnson, I.

A;Title: The MEL gene: a new member of the RAB/YPT class of RAS-related genes.

A;Reference number: 158355; MUID:91360267; PMID:1886711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 IMDTAGQERFRITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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A,Molecule type: mRNA
A,Residues: 1-206 <RES>
A,Cross-references: GB:S53270; NID:g234747; PIDN:AAB19682.1; PID:g234748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Indels
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                                               181 RMRASNELALAE-LEEEGKPEGPANSSK 208
                                                                                               ----NENSLQEAVDKLKSPPKKPSQKKK 200
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tes 93; Conservative
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A;Residues: 1-200 <ELF>
A;Cross-references: GB:M83677
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C, Genetics: A, Gene: MEL

Matches

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GTP-binding protein-like - Arabidopsis thaliana
MAlternate names: protein F1284.300
C;Alternate names: protein F1284.300
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: 14373
R;Bevan, M; Pohl, T; Weizenegger, T; Bancroft, 1.; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Database, March 2000
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                                                                                                                                                                                                                                 A;Reference number: Z24492
A;Accession: T48378
                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-216 <BEV>
                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
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                                                                                                              A,Map position: 1
A,Introns: 43/1; 147/2; 173/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
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C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Reywords: GTP binding; membrane protein; nucleotide binding; P-loop
F;16-131/Domain: translation elongation factor Tu homology <ETU>
F;12-29/Region: nucleotide-binding motif A (P-loop)
F;128-131/Region: GTP-binding NKXD motif
F;159-161/Region: GTP-binding SAK/L motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 -BEGKROVGREGGGOLAKEYGMDFYETSACTNINIKESF-----TRLTELVLQAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                    60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                               120 GNKADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
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                   A,Cross-references: EMBL:U80033; PIDN:AAC48200.1; GSPDB:GN00019; CESP:T23H2.5 A;Experimental source: strain Bristol N2; clone T23H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Title: The patterns of gene expression in the tomato shoot apical meristem. A,Reference number: S33899; MUID:93222691; PMID:8467223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MARREYDMLFKLLLIGDSGVGKTCLLYRFSDDAFNTTFISTIGIDFKIKTIELKGKKIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                         46.5%; Score 514; DB 2; Length 201; ilarity 46.9%; Pred. No. 8e-34; Conservative 48; Mismatches 51; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X69980; NID:g313028; PIDN:CAA49600.1; PID:g313029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.3%; Score 512; DB 2; Length 216; 50.5%; Pred. No. 1.3e-33; Attive 41; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 LRMRASNELALAELEEEGKPEGPANSSKTCWC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKMPDSTD----EQSRDTVNPVQPQRQSSSGGC 200
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EPQSIRINQSDQAGTA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99; Conservative
                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-216 <FL2>
A; Residues: 1-201 < WAM>
                                                                                          A; Gene: CESP: T23H2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S33900
                                                                  C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
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GTP-linding protein ypt2 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Accession: S12790; S10493; T39214
R;Haubruck, H.; Engelke, U.; Mertins, P.; Gallwitz, D.
EMBO J. 9, 1957-1962, 1990
A;Title: Structural and functional analysis of ypt2, an essential ras-related gene in the A;Reference number: S12790; MUID:90269232; PMID:2112089
                                                                                                                                                                                                                      C;Superfamily: ras transforming protein; translation elongation factor Tu homology F;16-131/Domain: translation elongation factor Tu homology <FTU>
                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 AGQERFRIITTAYYRGAMGILLVYDVTDESSFNNIRNWMKNIEQHASDNVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 -BEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESF-----TRLTELVLQAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 YDYLIKLLLIGDSGVGKSCLLLRFSDDTFTTSFITTIGIDFKIRTVELDGKRIKLQIMDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A;Residues: 1-200 <HAU>
A;Residues: references: BBL:X52469; NID:g5143; PIDN:CAA36707.1; PID:g5144
A;Croser-references: BS: Sweet, D.; Armstrong, J.
R;Fawell, E.; Hook, S.; Sweet, D.; Armstrong, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-200 «FMM»
A;Residues: 1-200 «FMM»
A;Crose-references: ERML:X52864; NID:95149; PIDN:CAA37045.1; PID:95150
R;MoDougall, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                       Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                 46; Indels
A;Cross-references: EMBL:AL162751
A;Experimental source: cultivar Columbia; BAC clone F12E4
                                                                                                                                        A;Introns: 25/1; 49/2; 83/1; 105/1; 137/3; 158/3; 189/3
A;Note: F12E4.300
                                                                                                                                                                                                                                                                                                                                       46.3%; Score 512; DB 2;
49.8%; Pred. No. 1.3e-33;
tive 43; Mismatches 46;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELEGLRMRASNELALAELEEE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 EPQGIKITKODTAASSSTAEK 209
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 49.89
Matches 100; Conservative
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, Cross-references: EMBL: 299262; PIDN: CAB16405.1; GSPDB: GN00066; SPDB: SPAC9E9.07c
A;Residues: 1-200 <MCD>
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Genetics:

A Gene: Ypt2
A, Gene: Ypt2
A, Map position: 1
A, Map position: 1
C, Superfamily: ras transforming protein; translation elongation factor Tu homology
C, Superfamily: ras translation elongation factor Tu homology «BTU»
F, 10-125, Domain: translation elongation factor Tu homology «BTU»
F, 16-23, Megion: uncleotide-binding motif A (P-loop)
F, 122-125, Region: GTP-binding NKXD motif
F, 152-154, Region: GTP-binding SAK/L motif
F, 199, 200/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

8; Gaps Query Match

46.2%; Score 510; DB 2; Length, 200;
Best Local Similarity 51.9%; Pred. No. 1.6e-33;
Matches 97; Conservative 39; Mismatches 43; Indels

63 DTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122

> 셤 ઠે 셤 ઠે 유

124 CDCEDQRQVSFEGGQALADELGVKFLEASAKTNVNVDEAFFTLA-----REIKKQK1 175

183 RASNELA 189

176 DAENEFS 182

Search completed: March 15, 2004, 11:16:52 Job time : 21 secs

us-09-817-198c-2.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 15, 2004, 11:09:18; Search time 18 Seconds (without alignments) 613.271 Million cell updates/sec

US-09-817-198C-2

Title: Perfect score:

1105 1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC 212 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		mus			-		P22127 discopyge o	_		Q92930 homo sapien		_				•	•		_	P16976 zea mays (m	-	-	Q9h0u4 homo sapien		_	_		P31584 volvox cart	3 neurosp	014462 candida alb	7	1560	P10536 rattus norv
SUMMARIES	ΩI	RB15 HUMAN	RB15 MOUSE	RB15_RAT	RABS HUMAN	RABS DISOM	RB13_HUMAN	RB10_DISOM	RB10_CANFA	RB10_HUMAN	RB8B_HUMAN	RB8B_RAT	RAB8_MOUSE	YPT2_SCHPO	RAB1_BETVU	ARA3_ARATH	YPT2_VOLCA	RB10_RAT	RYL1_YARLI	SAS1_DICDI	YPT1_MAIZE	RIC1_ORYSA	SAS2_DICDI	RB1B_HUMAN	RB35_HUMAN	YPT1 CHLRE	YPT1_PHYIN	ARAS ARATH		YPT1 NEUCR	SEC4 CANAL	YPT2_MAIZE	SEC4_YEAST	RB1B_RAT
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	Length	212	212	212	207	210	203	200	200	200	207	207	206	200	215	216	217	200	203	208	208	202	203	201	201	203	201	258	203	203	210	203	215	201
de	Query		98.6	97.5	49.3	48.8	48.1	48.1	48.0	48.0	47.8	47.8	47.6	46.2	46.1	46.0	45.7			43.8	43.7	43.4	43.3	43.3	43.2	•	43.2	43.1	43.0	43.0	42.8	42.6	42.6	42.4
	Score	1105	1090	1077	545	539.5	532	531.5	530.5	530.5	528.5	528.5	526	510	509	508	505.5	502.5	502	483.5	483	480	479	478.5	477.5	477.5	477	476	475.5	475	473	470.5	470.5	469
	Result No.	-	73	٣	4	'n	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	. 29	30	31	32	33

Q05974 lymnaea sta P05711 rattus norv	P11620 schizosacch P11476 homo sapien P22125 discopyge o	P01123 saccharomyc Q96e17 homo sapien O63482 mus musculu	Q9ulw5 homo sapien P51156 rattus norv	P25228 drosophila 095716 homo sapien
RAB1_LYMST RB1A_RAT	YPT1_SCHPO RB1A_HUMAN RAB1_DISOM	YPT1_YEAST RB3C_HUMAN RB3C_MOUSE	RB26_HUMAN RB26_RAT	RAB3_DROME RB3D_HUMAN
п п				
205	203 205 202	206	190	220
42.4	422.3 422.3	41.3	41.1	40.7
469 468	467 467 464	456.5 456.5 7.7.7	454.5	449.5 444.5
3.5 3.5	36 33 38	39 40 1	4.4	4 4 4 7

## ALIGNMENTS

s of synaptic vesicle membrane flow within the nerve terminal (By similarity). SIMILARITY: Belongs to the small GTPase superfamily. Rab family. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).

EMBL; AL139022; -; NOT ANNOTATED_CDS. Genew; HGNC:20150; RABIS. InterPro; IPR003579; GTPRASE RAb. InterPro; IPR003577; GTPRASE_RAS. InterPro; IPR003578; GTPASE_RAS. InterPro; IPR002041; RAN. 

us-09-817-198c-2.rsp

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212
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P35289;
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ID RB15
AC 9352
DT 01-F
DT 10-C
DE RAS-
GN RAB1
OS RAB1
OC EUK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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A strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A strausberg R.D., Colline F.S., Wagner L., Schemen C.M., Schuler G.D.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

A platchen M.J., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Woguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hillyk S.M.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1105; DB 1; Length 212; 100.0%; Pred. No. 5e-81; Ative 0; Mismatches 0; Indels 0;
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
S-geranylgeranyl cysteine
(By similarity).
S-geranylgeranyl cysteine
                                                                                                                                                                                                                                                                                                                                                                        (By similarity).
D16A0C71797ED782 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
20-CCT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-15.
                                                                                                                                                                                                                                                                                                                                                                                             212 AA; 24390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 212; Conservative
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                                                                                                                                                                                                                                                                                                                                                   212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                212
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Q8K386;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ID REIS MOUSE
ID REIS MOUSE
DT 28-FEB.
DT 10-CFB.
GN RABIS.
GN RABIS.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. C. Natl. Acad: Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May act in concert with RAB3A in regulating aspects of synaptic yesicle membrane flow within the nerve terminal (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                            similarity).
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.6%; Score 1090; DB 1; Length 212; 98.1%; Pred. No. 7.9e-80; ive 3; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP-binding; Lipoprotein; Frenylation; Protein transport.
NP BIND 15 22 GTP (BX SIMILARITY).
NP BIND 3 67 GTP (BX SIMILARITY).
NP_BIND 121 124 GTP (BX SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
S-geranylgeranyl cysteine
(By similarity).
S-geranylgeranyl cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iy similarity).
ESC492846DD47F12 CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RAB15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGT:1916865; 2310012606Rik.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR003578; GTPase_Rho.
InterPro; IPR002041; RAN.
InterPro; IPR01806; Ras trnsfrmng.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR001805; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00071, ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
SMART; SM00176; RAN; 1.
SMART; SM00173; RAS; 1.
SMART; SM00174; RHO; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC027769; AAH27769.1; -
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Matches 208; Conservative
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                                                                           STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=22210533; PubMed=1313420;
Elferink L.A., Anzai K., Scheller R.H.;
"Rabls, a novel low moleular weight GTP-binding protein specifically expressed in rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                     MEDLINE=93054572; PubMed=1429617;
Elferink L.A., Anzai K., Scheller R.H.;
Elferink L.A., Anzai K., Scheller R.H.;
-1. Biol. Chem. 267:22693-222693(1992).
-1. FUNCTION: May act in concert with RAB3A in regulating aspects of spraghtic vesicle membrane flow within the nerve terminal.
-1. TISSUE SPECIFICITY: Expressed predominantly in neural tissues.
-1. TISSUE SPECIFICITY: Expressed predominantly in neural tissues.
-1. SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
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GTGRPAMB; TIGR0231; small GTP; 1.

GTP-binding; Lipoprotein; Frenylation; Protein transport.

NP_BIND

NP_BIND

67

GTP (BY SIMILARITY).

NP_BIND

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GTP (BY SIMILARITY).

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GTP (BY SIMILARITY).
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INTERPROJ 19R003579; GTPASSE RAD.
INTERPRO, IPRO01806; RAS tringfrung.
INTERPRO; IPRO05225; SWall_GTP.
                                                                                                                                                                        Biol. Chem. 267:5768-5775(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMG.
SMART; SM00175; RAB; 1.
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                                                          SEQUENCE FROM N.A.
                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212
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207 AA

PRT;

STANDARD;

RABB_HUMAN ID RABB_HUMAN AC P24407;

RESULT 4

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SECTES=Human; TISSUE=Skin;

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Jordan H., Moore T., Mang J., Heiteh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.A., Gunnarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rocherch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91061765; PubMed-2123294;
Chavrier P., Vingron M., Sander C., Simons K., Zerial M.;
"Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Interacts with MAP4K2 and SYTL4 (By similarity).
                                                                                                                                                                                                                                                                                           Zahraoui A., Joberty G., Arpin M., Fontaine J.J., Hellio R., Tavitian A., Louvard D.; Tavitian A., Louvard D.; Tavitian A., Louvard D.; Tavitian B. Gypase is distributed in cytoplasmic vesicles in non polarized cells but colocalizes with the tight junction marker ZO-1 in polarized epithelial cells."; J. Cell Biol. 124:101-115(1994).
                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Brain;
Publ H.L. III, Ikeda S.R., Aronstam R.S.;
"CDNS of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91360267; Pubmed-1886711;
Nimmo E.R., Sanders P.G., Padua R.A., Hughes D., Williamson R.,
Johnson K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The MEL gene: a new member of the RAB/YPT class of RAS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Cell. Biol. 10:6578-6585(1990).-!- FUNCTION: May be involved in vesicular trafficking and neurotransmitter release.
                 01-WAR-1992 (Rel. 21, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Ras-related protein Rab-8 (Rab-8A) (Oncogene c-mel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                MEDLINE=94124602; PubMed=8294494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences.
(Rel. 21, Created)
(Rel. 21, Last seq
(Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene 6:1347-1351(1991)
                                                                                                      Homo sapiens (Human), and
                                                                                                                                                                                             CBI_TaxID=9606, 9615;
                                                                                                                            Canis familiaris (Dog)
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=Human;
                                                                                      WEL OR RABS
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MEDLINE=91115900; PubMed=1899244;
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P51153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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NP_BIND
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NKADEEOKROVGREOGQOLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Torpediniformes, Narcinoidei, Narcinidae, Discopyge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
S-GPETALYJGGTANY).
S-GPETALYJGGTANY, CYSTEINE
(BY SIMILARITY).
LEGNSPO -> WRATAP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.3%; Score 545; DB 1; Length 207; 52.9%; Pred. No. 1.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small GTP; 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA52DBF54A2CD056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
10-AUG-1991 (Rel. 19, Last sequence update)
10-CTZ-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-8 (ORA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003579; GTPase Rab.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PP00071; ras; 1.
                                                                                                                                                                         EMBL; X56741; CAA40065.1; -.
EMBL; S53266; AAB19691.1; -.
EMBL; AF498943; AAM21091.1; -.
EMBL; BC002977; AAM210977.1; -.
EMBL; X56385; CAB56776.1; -.
PIR; B49647; B49647.
HSSP; P05713; 3RAB.
Genew; HGNC:7007; MEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23668 MW;
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67
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TISSUE=Electric lobe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
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Matches
    REAL OCCOORDINATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IWDTAGQERFRITTAYYRGAMGIMKVYDITNEK&FDNIKDWIRNIEEHASSDVERMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NKADEEÇKROVGREÇGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Ngsee J.K., Elferink L.A., Scheller R.H.; "A family of ras-like GTP-binding proteins expressed in electromotor
                                                                                                                                               J. Biol. Chem. 266:2675-2680(1991).
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
S-gerant/Jegrantyl cysteine
(By similarity).
(By similarity).
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48.8%; Score 539.5; DB 1; Length 210;
Best Local Similarity 47.4%; Pred. No. 4.5e-36;
Matches 99; Conservative 56; Mismatches 45; Indels 9
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MEDLINE-94124602; PubMed=8294494;
Zahraoui A., Joberty G., Arpin M., Fontaine J.J., Hellio R.,
Tavitian A., Louvard D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ras related protein Rab-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 RMRASNELALAE-LEEEGKPEGPANSSK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 ----NENSLQEAVDKLKSPPKKPSQKKK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, M38391, AA49232.1; -.
PIR; B38625; B38625.
HSSP, POST13; 3RAB.
INCEPPRO; IPRO03579; GTPase Rab.
INCEPPRO; IPRO03579; GTPase Rab.
INCEPPRO; IPRO05225; SMall GTP.
PRINTS; PRO0449; RASTRNSFRNNG.
SWART; SMO0175; RAB; 1.
STGRFAMS; TIGR00231; SMall GTP; 1.
GTRP-binding; Prenylation; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24164 MW;
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ID RB13_HU
DC CCT;
DT 01-0CT;
DT 15-WAR-
DE RAB13.
OC ENLARY
CC ENLARY
CC ENLARY
CC MARMMALI:
OX NCB1_TR
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                                                                                                                                                                                                                                A REDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., H., Marny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski, M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

- I- FUNCTION: Could participate in polarized transport, in the assembly and/or the activity of tight junctions.

- II FUNCTION: Carbance C.M. Schart C.M. And And M. S. Bereblurk L.D. And And A. Schein J.S.A. 99:16899-16903 (2002).

- I- SUBCELLUIAR LOCATION: CYTOPLASM IN CELLS LACKING MITH THE CYTOPLASM IN CELLS LACKING MITH THE CYTOPLASM IN CELLS LACKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- TISSUE SPECIFICITY: Detected in several types of epithelia, including intestine, kidney, liver, and in endochelial cells. -1- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
"A small rab GTPase is distributed in cytoplasmic vesicles in non obtarized calls but colocalizes with the tight junction marker ZO-1 in polarized epithelial calls."; J. Cell Biol. 124:101-115(1994).
                                                                                                                Pull H.L. III, Ikeda S.R., Aronstam R.S., signal transduction "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM, 602672; -... Gridght junction; TAS. GO:0003923; Critight junction; TAS. GO:0003928; F:RAB small monomeric GTPase activity; TAS. GO; GO:000155; P:cell adhesion; TAS. GO; GO:001152; P:cell adhesion; TAS. InterPro; IPR001579; GTPase Rab. InterPro; IPR001806; Ras trisffamig. InterPro; IPR001805; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP-binding; Lipoprotein; Frenylation; Protein transport.
NP BIND 15 22 GTP (BY SIMILARITY).
NP BIND 63 67 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIGRFAMS; TIGR00231; small GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X75593; CAA53266.1; -.
EMBL; AF498948; AAM21096.1; -.
EMBL; BC000799; AAH00799.1; -.
PIR; A49647; A49647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:9762; RAB13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIGHT JUNCTIONS.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                         TISSUE=Placenta;
                                                                                                       TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                         61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKAYDHLFKLLLIGDSGVGKTCLIIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKIKLQ 60
                                                                                                                                                                                                                                                                                    1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUB-Electric lobe,
TISSUB-Electric lobe,
MEDLINE-91115900, PubMed=1899244;
MGBCL N.E., Elferink L.A., Scheller R.H.;
"A family of ras-like GTP-binding proteins expressed in electromotor neurons.",
7. Biol. Chem. 266:2675-2680(1991).
--- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Torpediniformes, Narcinoidei, Narcinidae, Discopyge.
                                                                                                                                                                                                                              18;
                     EFFECTOR REGION (BY SIMILARITY). S-geranylgeranyl cysteine
                                                                                                                                                                     DB 1; Length 203;
                                                                                                                                                                                                                              43; Indels
                                                                              (By similarity).
141621CB998178DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-geranylgeranyl cysteine
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16 23 GTP (BY SIMILARITY).
NP BIND 64 68 GTP (BY SIMILARITY).
NP_BIND 122 125 GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                     48.1%; Score 532; DB 1;
47.6%; Pred. No. 1.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Biscopyge ommata (Electric ray).
                                                                                                                                                                                                                              49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RMRASNELALAELEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 GRRSGN-----GNKP--PSTDLKTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M38390; AAA49230.1; -.
PIR; A38625; A38625.
HSSP; P05713; 3RAB.
InterPro; IPR001806; Ras trinsfrmng.
InterPro; IPR001806; Ras trinsfrmng.
InterPro; IPR002255; Small_GTP.
Pfam; PF00071; ras; 1.
PINTS; PR00449; RASTRNSFRMNG.
SWART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00231; small GTP; 1.
                                                                                                               203 AA; 22774 MW;
                                                                                                                                                                                                                              Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RB10 DISOM
P22127;
                                                                                                               SEQUENCE
                                                                                                                                                                        Query Match
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NP_BIND
NP_BIND
                                                                                                                                                                                                      Best Local
                                                         LIPID
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SPECIES=Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RB10 HUMAN
                      SEQUENCE
                                                               Query Match
                                                                                                          Matches
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                                                                                                                                                                                                                                                                                    60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                23
                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                             1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                         1 MAKKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTFISTIGIDFKIKTVELHGKKIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91061765; PubMed=2123294;
Chavrier P., Vingron M., Sander C., Simons K., Zerial M.;
"Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell
                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Céll. Biol. 10:6578-6585(1990).
--- PUNCTION: May be involved in vesicular trafficking and neurotransmitter release.
--- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                        120 GNKADBEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
SFRECTOR REGION (BY SIMILARITY).
SFGEANLY] Geranyl cysteine
(By similarity).
S-geranylgeranyl cysteine
                                                                                                            Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTP-binding; Lipoprotein; Frenylation; Protein transport.

NP BIND 16 23 GTP (BY SIMILARITY).

NP_BIND 64 68 GTP (BY SIMILARITY).

NP_BIND 12 125 GTP (BY SIMILARITY).

DOMAIN 38 46 EFFECTOR REGION (BY SIMILARI
                                                                                                                                                     30; Indels
             'cy almitatity'.
S-geranylgeranyl cysteine
(By similarity).
41D38E3D760519C5 CRC64;
                                                                                                        ch 48.1%; Score 531.5; DB 1; Similarity 56.4%; Pred. No. 1.8e-35; 97; Conservative 44; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-10.
    (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X56387; CAA39798.1; -.
PIR; D36364; D36364.
HSSP; P05713; 3RAB.
INTECPTO; IPRO03579; GTPASE_RAB.
INTECPTO; IPRO01806; Ras trnsfrmug.
INTECPTO; IPRO05225; Small_GTP.
Pfam; PP00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMB; TIGR00231; small_GTP; 1.
                                                                   200 AA; 22623 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog).
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68
125
46
199
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                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200
                           199
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                                                                   SEQUENCE
                                                                                                              Query Match
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                           LIPID
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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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                                                                                                                                                                                                                                                                              9
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MEDLINE=20402571; PubMed=10931946;

Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,

Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,

Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,

Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,

Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;

"Gene expression profiling in the human hypothalamus-pituitary-adrenal
axis and full-length cDNA cloning.";

Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T., Otsuki T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara P. Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.; "NEDO human cDNA sequencing project."; submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-Human, TISSUB-Brain,
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
Figha clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         1;
                                                                                              Length 200;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wong K., Hong W., Tang B.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
(By similarity).
22569 MW; 5D52B8E8E47D4362 CRC64;
                                                                                           Score 530.5; DB 1;
Pred. No. 2.2e-35;
6; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          088386; Q9D7X6;
15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UAR-2004 (Rel. 43, Last annotation update)
15-MAR-2014 (Rel. 43, Last annotation update)
RAB10.
                                                                                                                                                         46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES-Human; TISSUE=Cervix;
                                                                                              48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human), and
                                                                                                                                                               96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606, 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Mouse)
                                       200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Stomach;

KAWAN JO., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Enkunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Gaavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Gaavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Gaavant T.,

Sakai K., Okido T., Furuno M., Carninci M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fulits M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fulits M., Gariboldi M.,

Austincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazametts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

"Thurtional annotestion of a full-length mouse cDNA collection.",

Nature A. Ostaka K., Wang K.H., Naturne CDNA collection.",
MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Diatchenco, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenco, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapletcon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sannhez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Human and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
-!- FUNCTION: May be involved in vesicular trafficking and neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=Mouse; Zeng Q., Tan Y.H., Hong W.; Zeng Q., Tan Y.H., Hong W.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF106681; AAD43034.1; -. EMBL; AF297660; AAG13413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK023223; BAB14474.1;
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Genew; HGNC:9759; RAB10. MGD; MGI:105066; Rab10. InterPro; IPR003579; GTPase Rab.

EMBL, BC000896; AAH00896.1; -EMBL, AR035646; AAC29313.1; -EMBL, AK008725; BAB25858.1; -HSSP; PO5713; 3RAB EMBL; AF498945; AAM21093.1;

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61 QIWDTAGQERFHIITISYYRGAMGIMLVYDIINGKSPENISKWLRNIDEHANEDVERMLL 120
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MEDLINE=22388257, PubMed=12477932;

MEDLINE=22388257, PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R.Lausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hasheh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshlywis S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                     GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
STPECTOR REGION (BY SIMILARITY).
S-gerantylgeranyl cysteine
(By similarity).
                                                                                                                                                                                                                                                                                                                                                            48.0%; Score 530.5; DB 1; Length 200; 55.8%; Pred. No. 2.2e-35; Live 46; Mismatches 29; Indels 1;
                                                                                                                         transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seki N., Saito T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                      S-geranylgeranyl cysteine (By similarity).
                                                                                                                                                                                                                                                                                            PY BIMITALLY).
| -> H (IN REF. 7).
| 7F02B8E8E46EE1E8 CRC64;
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                                                                                                                                                                                                                                                                                                      N -> H (IN REF
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR00525; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRNNG.
SMART; SM00175; RAB; 1.
TIGR0AB; TIGR00231; small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Pro
                                                                                                                                                                                                                                                                                                                         22541 MW;
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                                                                                                                                              23
68
125
199
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200 AA;
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38
199
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DOMAIN
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us-09-817-198c-2.rsp

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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                     SEQUENCE FROM N.A.
MEDLINE=96393028; PubMed=8799816;
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HSSP; P05713; 3RAB.
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Best Local Similarity
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                     NCBI_TaxID=10116;
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01-OCT-1996 (
01-OCT-1996 (
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NP_BIND
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                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IWDTAGGERFRITTAYYRGAMGIMLVYDITNEKSFDNIKNWIRNIEBHASSDVERMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen D., Guo J., Gahl W.A.;
"RAB GTPases expressed in human melanoma cells.";
Biochim. Biophys. Acta 1355:1-6(1997).
-!- FUNCTION: May be involved in vesicular trafficking and neurotransmitter release (By similarity).
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.8%; Score 528.5; DB 1; Length 207; 54.0%; Pred. No. 3.3e-35; tive 47; Mismatches 33; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003928; F:RAB small monomeric GTPase activity; NAS. GO; GO:0015031; P:Protein transport; NAS. InterPro; IPR003579; GTPase Rab. InterPro; IPR001806; Ras trinsfrung. InterPro; IPR005225; Small_GTP.
                                 numan and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-8B.
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                                                                                                                   AEDLINE=97182150; PubMed=9030196;
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB038995; BAA92249.1; -. EMBL; BC020654; AAH20654.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U66624; AAC51199.1; -. HSSP; P05713; 3RAB.
                                                                                   SEQUENCE OF 67-119 FROM N.A.
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les 95; Conservative
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P70550;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@ibb_sib.ch).
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Armstrong J., Thompson N., Squire J.H., Smith J., Hayes B., Solari R., "Identification of a novel member of the Rab8 family from the rat basophilic leukaemia clilline, RBL.2H3.";
J. Cell Sci. 109:1265-1274(1996).
-!- FUNCTION: May be involved in vesicular trafficking and neurotransmitter release (By similarity).
-!- TISSUE SPECIFICITY: Highest levels of expression in the spleen, testis and brain.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

S-geranylogeranyl cysteine

(By similarity).
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InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001805; Ras trinsfrung.
InterPro; IPR001825; Small_GTP.
Pfan; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRNG.
SMART; SM0175; RAB; 1.
TIGREAMs; TIGR00231; small_GTP, 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport.
NP_BIND.
NP_RIND.
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-8 (Oncogene c-mel).
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01-AUG-1990
10-OCT-2003
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                                    SCHPO
            YPT2_SCHPO
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 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                "SIP4 a/granuphilin-a inhibits dense-core vesicle exocytosis through interaction with the GDP-bound form of Rab27A in PC12 cells."; J. Biol. Chem. 278:15390-15396 (2003).
-!- PUNCTION: May be involved in vesicular trafficking and neurofransmitter release.
-!- SUBUNIT: Interacts with MAP4K2 and SYTL4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                          STRAIN-BALB/c; TISSUE-Melanoma;
MEDLINE-96209873; PubMed-8643544;
Ren M., Zeng J., De Lemos-Chiarandini C., Rosenfeld M., Adesnik M.,
                                                                                                                                                                                                        "In its active form, the GTP-binding protein rab8 interacts with a stress-activated protein kinase.";
Proc. Natl. Acad. Sci. U.S.A. 93:5151-5155(1996).
MEDLINE=91360267; PubMed=1886711;
Nimmo E.R., Sanders P.G., Padua R.A., Hughes D., Williamson R.,
Johnson K.J.;
                                                    "The MEL gene: a new member of the RAB/YPT class of RAS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

S-geranylgeranyl cysteine
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GTP-binding; Prenylation; Lipoprotein; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3y similarity).
49D832725D662942 CRC64;
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GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR0013579; GTPase Rab.
InterPro; IPR001806; Ras trinsfrung.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; I.
PRINIS; PR00449; RASTRNSFRMNG.
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MEDLINE=22590467; PubMed=12590134;
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HSSP; P05713; 3RAB.
                                                                                     Oncogene 6:1347-1351(1991).
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Best Local Similarity 56.**.
Best Local 93; Conservative
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                                                                                                                        INTERACTION WITH MAP4K2
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67
124
45
203
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Sabatini D.D.;
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121 NKADEEÇKRQVGREÇGQQLAKEYGMDFYETSACTNINIKESFTRL 165

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                                                                                                                                                                      Hengst L., Lehmeier T., Gallwitz D.; "Structural and functional analysis of ypt2, an essential ras-related gene in the fission yeast Schizosaccharomyces pombe encoding a Sec4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- MISCELLANEOUS: This protein is essential for cell viability.
                                                                                                                                                                                                                                                            Fawell B., Hook S., Sweet D., Armstrong J.;
"Novel YPT1-related genes from Schizosaccharomyces pombe.";
Nucleic Acids Res. 18:4264-4264 (1990).
                                                             YPTZ OR SPAC9E9.07C. Schizosacharomyces pombe (Fission yeast).
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetales; Schizosaccharomycetes; Schizosaccharomycetaces.
                   01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
200 AA.
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                                                    Ras-related protein ypt2.
                                                                                                         Schizosaccharomyces
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                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                       protein homologue.
                                                                                                                     NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 MDESKRAVPTAKGQALADEYGIKFFFTSAKTNINVEEVFFSIARDIKQ--RLADSDTRQE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
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Gene 108:259-264(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN=cv. Landsberg erecta, cv. Columbia, cv. En-1, cv. Lapalmam,
and cv. Estland;
TISSUE=Loaf;
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Matsui M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
46.1%; Score 509; DB 1; Length 215;
Best Local Similarity 47.8%; Pred. No. 1.2e-33;
Matches 100; Conservative 42; Mismatches 59; Indels
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

S-geranylgeranyl cysteine
(By similarity).

S-geranylgeranyl cysteine
(By similarity).
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Arabidopsis thaliana (Mouse-ear cress).
      and this statement is not removed.
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                                                                                                                           EMBL, Z49152; CAA89021.1; -...
PIR; T14565; T14565.
HSSP; POST13; BRAB.
InterPro; IPR003579; GTPase Rab.
InterPro; IPR001806; Ras trinsfrang.
InterPro; IPR001806; Ras trinsfrang.
InterPro; IPR001806; Ras trinsfrang.
InterPro; IPR001225; Small_GTP.
Pfan; PF00071; ras; I.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SW00175; RAB; 1..
GTP-binding; Lipoprotein; Prenylation.
NP_BIND 70 74 GTP (BY SIMI NP_BIND 70 74 GTP (BY SIMI LIPID 128 112 S-geranylger
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STRAIN=cv. Columbia;
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STRAIN=CV. D100 KS 38080;
MEDLINE=96307523; PubMed=8680960;
MEDLINE=96307523; PubMed=8680960;
Molecular Cloning and structural analysis of cDNAs that encode 3 small GTP-binding proteins from sugar beet.";
C. R. Acad. Sci., III, Sci. Vie 319:91-97(1996).
C. R. Acad. Sci., III, Sci. Vie 319:91-97(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
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Best Local Similarity 51.9%; Pred. No. 9.5e-34;
Matches 97; Conservative 39; Mismatches 43; Indels
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GTP (BY SIMILARITY).
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
S-GERGION (PROBABLE).
S-GERGION (PROBABLE).
(By similarity).
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S-geranylgeranyl cysteine
Stay similarity).
2C658D153A290C30 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                             Geneba SPonde, SPAC9E9.07c; -.
InterPro; IPR001805; Ras trnsfrang.
InterPro; IPR001805; Ras trnsfrang.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRANG.
SMART; SM00175; RAB; 1.
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EMBL; X52469; CAA36707.1; -. EMBL; X52864; CAA37045.1; -. EMBL; Z99262; CAB16405.1; -.
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HSSP; P05713; 3RAB.
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Ratmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomench P.,
Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomench P.,
Ra Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Banger F.,
Ra Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Bangert S.,
Wurmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G.,
Ra Wichelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Ra Worzer D., Collado M., Pallavicini A., Toppo S., Simionati B.,
Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Ravarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,
Ravarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,
Rayer K., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
A Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
Rayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Rayer K.F.X., Naters A., Utterback T., Fujila C.Y., Shea T.P.,
Raser C.M., Walte R., Utterback T., Fujila C.Y., Shea T.P.,
Parser C.M., Walte R., Utterback T., Fujila C.Y., Shea T.P.,
Raser C.M., Kaneko T., Idesawa K., Kawashima K., Kaneko T., Matsumo A., Muraki A.,
Riyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Riyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Ryokawa C., Kamada M., Yasuda M., Tabata S.,
Ryotuene and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@isb-sib.ch).
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InterPro; IPR001806; Ras trnsfrung.
InterPro; IPR005225; Small_GTP.
Pfam; PP00071; ras; 1.
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SMART; SM00175; RAB; 1.
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MEDLINE=21016720; PubMed=11130713;
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PIR; JS0640; JS0640.
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Search completed: March 15, 2004, 11:15:20 Job time : 18 secs

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Q8iw89 homo sapien
Q7t3a4 brachydanio
Q9ty82 caenorhabdi
Q15971 drosophila
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Q9het4 aspergillus
Q24466 arabidopsis
Q40218 lotus japon
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Q9fjf1 arabidopsis
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| Q94148 caenorhabdi<br>Q40219 lotus japon<br>Q8vwf9 nicotiana t<br>Q84ta8 oryza sativ<br>Q40177 lycopersico |                                               | Q8W3J3 nicotiana t<br>Q96362 brassica ca<br>Q86V13 colletotric<br>Q81bq4 arabidopsis<br>Q9swV8 lycopersico<br>Q41024 pisum sativ |                                                          | Q40569 nicotiana t<br>Q26554 schistosoma<br>Q8ru63 oryza sativ<br>Q9zrh6 petunia hyb<br>Q9hdt5 trichoderma<br>Q39845 glycine max |
|------------------------------------------------------------------------------------------------------------|-----------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|
| Q94148<br>Q40219<br>Q8VWF9<br>Q84TA8<br>Q40177                                                             | 040217<br>084314<br>098791<br>041023<br>04944 | Q8W3J3<br>Q96362<br>Q96VL3<br>Q8LBQ4<br>Q9SWV8                                                                                   | 096GU4<br>08W3J2<br>041022<br>09C1Z5<br>041061<br>09BLF3 | 040569<br>026554<br>028RU63<br>09ZRH6<br>09HDT5                                                                                  |
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## ALIGNMENTS

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RESULT 1

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TO 10-DEC-2001 (TERMBLrel. 19, Created)

TO 10-DEC-2001 (TERMBLrel. 19, Last sequence update)

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                                                                                                                                                                                                                             61 IWDTAGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWYSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                   61 IWDTAGOERYQTITKQYYRRAQGIFLUYYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDE------VG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strauberg R.;
Strauberg R.;
Strauberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC040679; AAH40679.1;
GO; GO:0003525; F:GTP binding; IEA.
GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.
GO; GO:0003930; F:RAS small monomeric GTPase activity; IEA.
GO; GO:0003931; F:Rho small monomeric GTPase activity; IEA.
GO; GO:00008886; P:intracellular protein transport; IEA.
GO; GO:000026886; P:intracellular protein transport; IEA.
GO; GO:00002689; P:small GTPase mediated signal transduction; IEA.
GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
                                                                                                                                1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIDVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MAKQYDVLFRLILLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 63
                                                                                                    1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                      ö
Query Match
72.2%; Score 798; DB 11; Length 168;
Best Local Similarity 99.3%; Pred. No. 5.2e-60;
Matches 152; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%; Score 573; DB 4; Length 211; 62.8%; Pred. No. 9e-41; tive 15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA; 23761 MW; 3BFA7CF89D4DF54F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                  121 NKADEBOKRQVGREQGQQLAKEYGMDFYETSAC 153
                                                                                                                                                                                                                                                                                                                                                   121 NKADEEQKROVGREOGOOLAKEYGMDFYETSAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMB; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002041; RAN.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein (Fragment).
Homo sapiens (Human).
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GTPase Rho.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003579; GTPase Rab.
InterPro; IPR003577; GTPase Ras.
InterPro; IPR003578; GTPase Rho.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0449; RASTRNSFRMNG.
SWART; SM00175; RAB; 1.
SWART; SM00173; RAS; 1.
SWART; SM00173; RAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.8%
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00071; ras; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEOUENCE
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MEDLINE=2238825; PubMed=12477932;

MEDLINE=2238825; PubMed=12477932;

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A latestul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A latestul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Britchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan B.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A lones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse C.D.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 INDIAGOERYQTITKOYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQXILIG 120
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                                        1 MAKKYDFLFKLLLIGDSGVGKTCLIRFAEDNFNSTYISTIGIDFKVKTIEVEGKKVKLQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R^{\perp}_{i}, Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC053195; AAH53195.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 200 AA, 22458 MW; FA177CEDAEF2820C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Mismatches
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121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep; D1037.4; CE30373.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.

GO; GO:00015031; P:PROTE in transport; IEA.

GO; GO:0007264; P:Small GTPase mediated signal transduction; IEA.

GO; GO:000160; P:two-component signal transduction; IEA.
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                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genome sequence of the nematode C. elegans: a platform for investigating biology, The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; AF106592; AAK21367.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.4%; Score 557; DB 5; Length 211; Best Local Similarity 55.0%; Pred. No. 2.1e-39; Matches 104; Conservative 42; Mismatches 39; Indels
                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
C. elegans RAB-8 protein (corresponding sequence D1037.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ledwith J., Biewald T., "The sequence of C. elegans cosmid D1037."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; P. 200675; SIGMAS4_INTERACT_1; 1.
GTP-binding; Lipoprotein.
SEQUENCE 211 AA; 24022 MW; B7609A91B6082DA2 CRC64;
                                                                   211 AA.
                                                                                                                                                                                                                                                                                                                                             Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
Pfam; PR00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001806; Ras trnsfrmng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003579; GTPase Rab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology. The C. Science 282:2012-2018(1998).
                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 RMRASNELA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 EMRAGGSVS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
                                                                   Q9TYS2
RESULT 4
Q9TYS2
                                                                                                     A CONTRACTOR OF A CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CON
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.P.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.P.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.P.,
Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
R.A. Sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.E., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Beeson K.Y., Basu A. Baxendale J., Baytaktargoll L., Beasley E.M.,
Beeson K.Y., Banca P.V., Berman B.P., Bhandari D., Bolchtakov S.,
R. Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Aberry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R. Borkova D., Boupler A., Dang Z., Mays A.D., Davies P.,
Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
B. Dodgon K.J. Evones M., Dugan-Rocha S., Pleietz R.M.,
R. Posler C., Gabriellan A.E., Garriellan A.E., Mulland T.J., Weil M.-H., Ibegwam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alako P., Lei Y., Levitsky A.A., Li J., Willy M.-H., Ibegwam C.,
Alako P., Lei Y., Levitsky A.A., Li J., Waller B.E., Mount S.M. Wollson K.A., Nixon K., Murphy L., Muzny D.M., Nelson D.L.,
Alaracolo M., Pittema G.S., Pan S., Pollard J., Wang X.,
Alaracolo M., Pittema G.S., Pan S., Pollard J., Wang X.,
And S., Wassamman G.S., Pan S., Pollard J., Wang X.,
Andre S., Wassamman D.A., Weinfercok M., Wang M., Waller S., Siden K., Wassaman S.,
Alaracolo M., Wassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Satoh A.K., Tokunaga F., Ozaki K.;
"Rab proteins of Drosophila melanogaster: novel members of the Rab-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                          Last sequence update)
Last annotation update)
                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-OREGON R; TISSUE=Head;
MEDLINE=97228579; PubMed=9074639;
                                                                                                                                                    RAB10 protein (LD39986P).
RAB10 OR DRAB10 OR CG17060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EBS Lett. 404:65-69(1997).
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                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         WCBI_TaxID=7227;
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                                         015971
RESULT 5
                       015971
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61 INDTAGOERYOTITKOYYRRAQGIFLUYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NKADEBOKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NKCDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIKAKMDKKLEGN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAXTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQ 60
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF52580; AAM82581;
GO; GO:0003525; F:GTP binding; IEA.

GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.

GO; GO:0003931; F:RAS small monomeric GTPase activity; IEA.

GO; GO:0003931; F:RAS small monomeric GTPase activity; IEA.

GO; GO:0000588; P:Intracellular protein transport; IEA.

GO; GO:0007264; P:small gTPase mediated signal transduction; IEA.

GO; GO:000166; P:wo-component signal transduction system (p. .; IEA.

InterPro; IPR006688; ARF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
     transcriptome based on functional annotation
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Lau A.S.N., Cheng C.Y., Mruk D.D.;
"Rabi3 participates in Sertoli cell tight junction assembly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                     BELONGS TO THE RAB SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.0%; Score 541; DB 11; Length 207; 50.3%; Pred. No. 4.6e-38; ive 49; Mismatches 49; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP-binding; Lipoprotein. SEQUENCE 207 AA; 23668 MW; AC89DC85588FB8F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0449; RASTRNSFRANG.
SMART; SM00175; RAB; 1.
TIGRFAMB; TIGR00231; Bmall GTP; 1.
PROSITE; PS00675; SIGMAA4 INTERACT 1; 1.
                                                                                                                                                                                                                                                      GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR003579; GTPasse_Rab.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
PERM; PF00071; ras; 1.
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                                                                                -i- SIMILARITY: TO RAS PROTEINS.
EMBL, BC019990, AAH19990.1; -.
EMBL, AK076048; BAC36146.1; -.
EMBL; AK079306; BAC37603.1; -.
EMBL; AK080740; BAC38003.1; -.
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RMRASNELALAELEEEE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SPQGSSHGVKITVEQQK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel, 22, 01-0CT-2002 (TrEMBLrel, 22, 01-0CT-2003 (TrEMBLrel, 25, GTP-binding protein RAB13.
        "Analysis of the mouse trans
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 50.3%;
les 99; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                                           MGD; MGI:96960; Mel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBK3X5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8K3X5
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Matches
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        SW DER BERRY SON SERVICE STATE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE SON SERVICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNEKSFENIVKWLRNIDEHANEDVEKMIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GNKADEBOKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
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                                                                                                                                                                                FlyBase; FBgn0015789; Rablo.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0005225; F:GTP binding; IEA.

GO; GO:0001928; F:RAB small monomeric GTPase activity; IEA.

GO; GO:00015031; P:Protein transport; IEA.

GO; GO:0007264; P:Small GTPase mediated signal transduction; IEA.

GO; GO:000160; P:two-component signal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKKTYDLLFKLLLIGDSGVGKTCLLFRFSDDAFTSTFISTIGIDFKIKTVELRGKKIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5, Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to mel transforming oncogene (Perived from cell line NK14)-RAB8 homolog (Cell line NK14 derived transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREPMS; TIGR00231; small GTP; 1.
PROSITE; PS00675; SIGMAS4 INTERACT 1; 1.
GTP-binding; Lipoprotein.
SEQUENCE 204 AA; 23336 MW; 4E058761C6854920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUB=Body, Cerebellum, and Retina; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.5%; Score 546.5; DB 5
49.8%; Pred. No. 1.5e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 AA
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003579; GTPase Rab.
InterPro; IPR001806; Ras trnsfrmug.
InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
Pfam; PP00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                EMBL; AE003572; AAF50924.1; -. EMBL; AB006189; BAA21744.1; -. EMBL; AY060425; AAL25464.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00449; RASTRNSFRMNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 49.88 Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00175; RAB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                P05713; 3RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Best Local &
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                                                                                                                                                                HSSP;
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'EBS Lett. 404:65-69(1997).
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S.A. Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelfer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Botchan M.R., Borner B.P., Bhandari D., Bolahakvo S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Dablos B., Delcher A., Downes M., Dusbin R.O., Dunn P.,
A durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                             61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                  121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                        1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                                     DB 11; Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila
                                                                                                                                                                                                                                                                              46; Indels
                                                                                                                                                                                                                           203 AA; 22901 MW; B6687462C6EA95A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RABS protein (LD44762p).
                                                                                                                                                                                                                                                   Query Match 47.8%; Score 528.5; DB 1
Best Local Similarity 48.1%; Pred. No. 5.2e-37;
Matches 100; Conservative 53; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 RSGNSSKPSSTDLKVSDKK----NSNK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMRASNELALAELEEEGKPEGPANSSK 208
                                                                                                                                                                          PROSITE, PSO0675; SIGMAS4_INTERACT_1; 1.
GPP-binding.
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                                                InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR002078; Sig54 interact.
InterPro; IPR002025; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                         GTPase_Rho.
             GTPase Ras
GTPase Rab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                SMART; SM00177; ARF; 1.
SMART; SM00175; RAB; 1.
SMART; SM00176; RAB; 1.
SMART; SM00173; RAS; 1.
SMART; SM00174; RHO; 1.
                         interPro; IPR003578;
                                      InterPro; IPR002041;
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                                                                                                                                                                                                                            SEQUENCE
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PROBLET C. GORDE P. GORTELI J.H., CHE N. E., GORDEN, W. GLAGGER, K. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORTELI J.H., CH. E., CHANGE, C. GORDEN, C. GORTELI J.H., CH. C. C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. GORDEN, C. M. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILLING, C. MILL
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NCBI_TaxID=10090;
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                                                                                      09DD03
                                           RESULT 10
Q9DD03
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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003282; F:GTP binding; IEA.
GO; GO:0003282; F:RAB small monomeric GTPase activity; IEA.
GO; GO:0015031; P:protein transport; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
GO; GO:000160; P:two-component signal transduction system (p. .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTFISTIGIDFKIKTVELQGKKIKL
                                                               NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GNKADEBOKROVGREQGOQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.W., Otterwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Trampe J., Heubner D., Mambutt R., Korn B., Klein M., Poustka A.; Arampe J., Heubner D., Manlysis of S00 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00231; small GTP; 1.
PROSITE; PS00675; SIGMAS4 INTERACT 1; 1.
Hypothetical protein; GTP-binding; Lipoprotein.
SEQUENCE 200 AA; 22469 MW; 7F01DB88E46EE3EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.6%; Score 526.5; DB 4
55.8%; Pred. No. 7.5e-37;
tive 45; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                     Created)
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InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=21154917; PubMed=11230166;
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                                                                                                                                                                                                                                                                                                                                                 01-MAR 2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25, DKFZD564L1962.
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les 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                      181 RMRASN 186
                                                                                                                                                                                                 176 RMEANN 181
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                                                                                                                                                                                                                                                                                                                                   Q9H0T3;
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Matches
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Rawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Arawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Black J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Wandria H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.
GO; GO:0015031; P:protein transport; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
GO; GO:0000160; P:two-component signal transduction system (p. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
GTP-binding; Lipoprotein.
SEQUENCE 202 AA; 22770 WW; 5DF599432E228AC0 CRC64;
                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 0610007N03Rik protein (RIKEN cDNA 0610007N03 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.6%; Score 526; DB 11;
54.1%; Pred. No. 8.4e-37;
iive 45; Mismatches 33;
                                                                            Created)
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InterPro; IPR002078; Sig54 interact
InterPro; IPR005225; Small_GTP.
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0005525; F:GTP binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Kidney;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIGRFAMB; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003579; GTPase Rab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92; Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P05713; 3RAB.
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EMBL; JUBA11E OFF CLONES.";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

BMBL; Juba12966; CAB65088.1; -.

DR EMBL; AL32966; CAB65088.1; -.

DR EMBL; AL32966; CAB65080.1; -.

DR EMBL; AL32966; CAB67668.1; -.

DR EMBL; AL9501; T45901.

BRSP; P05713; 3RA94

GO; GO:000367; F:DNA binding; IEA.

GO; GO:000367; F:DNA binding; IEA.

GO; GO:0007264; P:Small dnonmeric GTPase activity; IEA.

GO; GO:000160; P:Wo-component signal transduction; IEA.

GO; GO:000166; P:wo-component signal transduction; IEA.

RO; GO:000166; Ras trnsfrmng.

InterPro; IPR001806; Ras trnsfrmng.

InterPro; IPR002078; Sigfall_GTP.

IREPRO; IPR002025; Small_GTP.

IREPRO; IPR002021; GMBL GTP.

IREPRO; IREPROSE SIGFAL GTP.

INTERPRO; IPR002078; Sigfall_GTP.
                                                                                                                                                                                                                                                                         Bloecker H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIWDT
           GTPase AERABS (At3g33610).

RABS OR F4P12 310.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II, Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan G.J., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kaniya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.;
Fraidmann K.;
Frull-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels
                                                                                                                                                                  SEQUENCE FROM N.A.
STRALI-G. Columbia;
Bischoff F., Palme K.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
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 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.0%; Score 519; DB 10;
llarity 51.9%; Pred. No. 3.6e-36;
Conservative 42; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGREAMS; TIGRO0231; small GTP; 1.
PROSITE; PSO0675; SIGMAS4_INTERACT_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation.";
Genome Biol. 0:0-0(2002)
 01-OCT-2003 (TrEMBLrel.
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Best Local Similarity
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                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                   61 VWDTAGQERFKTITTAYYRGAMGIILVYDITDEKSFENIQNWMKSIKENASAGVERLLLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 DTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTAGGERFRIITTAYYRGAMGILLVYDVTDERSFQNIRTWFSNVEQHASEGVHKILIGNK 124
                   IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Punt P.J., Seiboth B., Weenink X.O., van Zeijl C.M., Lenders M., Konetschny C., Ram A.F., Montijn R., Kubicek C.P.,
Van Den Hondel C.A.,
"Identification and characterisation of a family of secretion related small GTPase encoding genes from the filamentous fungus Aspergillus alumituted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL, AJ278658; CAC17832.1; --
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KOYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW
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                                                                                                                                                                                                                                                                                                                                                             Eukarjota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Burotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus,
NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:000525; F:GTP binding; IEA.
GO; GO:000525; F:GTP binding; IEA.
GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.
GO; GO:0015031; P:protein transport; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
InterPro; IPR003579; GTPase Rab.
InterPro; IPR001806; Ras trisfrmug.
InterPro; IPR005225; Small GTP.
                                                                                          121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVL 170
                                                                                                             47.1%; Score 521; DB 3; Length 206; 60.6%; Pred. No. 2.3e-36; Live 30; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP-binding; Lipoprotein. –
SEQUENCE 206 AA; 22823 MW; 501916B795CF8CBC CRC64;
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                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
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TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                        Secretion related GTPase, (SrgA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
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                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=N402;
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                                                                                                             PRELIMINARY;
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Sasaki T., Matsumoto T.
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01-NOV-1996
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                                                                                     RESULT 14
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Q40215
                                                                                                27XHP7
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                                    - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                     AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -EEOKROVGREGGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLOA----HRKELE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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YDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.
GO; GO:00015031; P:protein transport; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                            Borg S., Brandstrup B., Jensen T.J., Poulsen C.; "Identification of new protein species among 33 different small GTP-binding proteins encoded by CDNAs from Lotos japonicus, and expression of corresponding mRNAs in developing root nodules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDYLIKLLIGDSGVGKSCLLLRPSDGSPTTSPITTIGIDFKIRTIELDGKRVKLQIWDT
                       AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.9%; Score 518; DB 10; Leust.. --. 48.6%; Pred. No. 4.3e-36; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant J. 11:237-250(1997).
--- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
--- SEMBL; Z73947; CAA98175.1;
--- HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PRO0449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGREPARs; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIDAS4_INTERACT_1; 1.
GTP-binding; Lipoprotein.
SEQUENCE 214 AA; 23627 MW; 5ElA6E83505E50D7 CRC64;
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001806; Ras tringfrmng.
InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Root nodules;
MEDLINE=97231679; PubMed=9076991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003579; GTPase Rab
                                                                                                                                                                                                                                     01,
01,
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                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                        192 TIKINQSDQ 200
                                                                                                                         GLRMRASNE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00071; ras; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=34305
                                                                                                                                                                                                                                                                                                 Lotus japonicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                        65
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Q40218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AGQERFRIITTAYYRGAMGILLVYDVTDESSFNNIRWIRNIEQHASDNVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
132 MDESKRAVPTSKGQALADEYGIKFFETSAKTNLNVEEVFFSIARDIKQRLADTDHKAEPT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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MEDINE=97231679; PubMed=9076991;
Borg S., Brandstrup B., Jensen T.J., Poulsen C.;
Indentification of new protein species among 33 different small GTP-binding proteins encoded by cDNAs from Lotos japonicus, and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 YDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lotus japonicus.
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matbumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC clone:P0565A07.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005194; BAC80082.1; -.
SEQUENCE 215 AA; 23993 MW; F3DAD303C533C7EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 MDESKRAVPTSKGQALADEYGIXFFETSAKTNLNVEQVFFSIARDIKQ
                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ethylene-responsive small GTP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

46.9%; Score 518; DB 10;
Best Local Similarity 47.5%; Pred. No. 4.4e-36;
Matches 103; Conservative 42; Mismatches 48
                                                                                                                                         --- AANKSSCC 213
                                                                                                                                                                                                                                                                                                                            215 AA.
                                                                   179 GLRMRASNELALAELEEEGKPEGPANSSKTC
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us-09-817-198c-2.rspt

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125 -EEOKROVGREOGOOLAKEYGMDFYETSACTNINIKESFTRLTELVLOAHRKELEGIRMR 183
                                                                                                                                                                                                                                                                                         65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                           13 YDYLIKILLIGDSGVGKSCLLIRPSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIMDT 72
                                                                                                                                                                                                                  5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIBVDGIKVRIQIWDT
                                                                                                                                                                                                   7; Gaps
                                                                                                                                                                                  Query Match

46.7%; Score 515.5; DB 10; Length 216;
Best Local Similarity 48.3%; Pred. No. 7.1e-36;
Matches 100; Conservative 43; Mismatches 57; Indels 7;
                                                                                                                                                                                                                                                                                                               184 ASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                          A--EPQTIQINQPDASASGQAAQKSC 213
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2546.574 Million cell updates/sec
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1 MAKQYDVLFRLLLIGDSGVG......LEBEBGKPEGPANSSKTCWC 212
                                    March 21, 2004, 11:58:09; Search time 2486 Seconds
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                        BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                           US-09-817-198C-2
                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                     Sequence:
                                         Run on:
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55026578 27513289 segs, 14931090276 residues Total number of hits satisfying chosen parameters: Searched:

0.5 7.0

Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries

Command line parameters:
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-MODEL=frame+ pln.model -DEV=xlp
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-DB=EST -QPMT=fastap -SUFFIX=rst -MINNATCH=0.1 -LOOPCIL=0 -LOOPEXT=0
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

em\_estfun: \*
em\_estom: \*
em\_gss\_hum: \* em\_gss\_pro:\*
em\_gss\_rod:\*
em\_gss\_phg:\*
em\_gss\_vrl:\*
gb\_gssl:\* em gas inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* em\_gss\_fun:\* em gas mam:\* em\_gas\_mus:\* 1: em\_estba:\*
2: em\_esthum:\*
3: em\_estin:\*
4: em\_estin:\*
5: em\_estpl:\*
6: em\_estpl:\*
7: em\_estro:\* em\_htc:\*c gb\_est1:\* gb\_est2:\* gb\_est2:\* gb\_est4:\* EST: \* Database :

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Resul | ılt |       | *<br>Ouerv |               |    |          |             |           |
|-------|-----|-------|------------|---------------|----|----------|-------------|-----------|
| ~     | No. | Score | ch.        |               | DB |          | Description |           |
| i     | -   | 66    | 1.0        | 109           | 10 | 033      | 50330       | ø         |
|       | 7   | 988   | 6          | 0             | 13 | 784      | 17848       | AGENCOURT |
|       | m   | 953.5 | 86.3       | 932           | 10 | BF535642 | BF535642    | 602054039 |
|       | 4   | 8     | ٠.         | $\overline{}$ | 12 | 828      | 18588       | 603277781 |
|       | ហ   | 915.5 | ď          | 2             | 13 | 350      | 13508       | 603523088 |
|       | 9   | 91    | ä          | 9             | 10 | 173      | 01130       | 601753464 |
|       | ^   | 910   | ä          | 0             | 10 | 816      | 78163       | 601809083 |
|       | ω   | 885   | 。          | σ             | 12 | 793      | 57933       | 603237549 |
|       | σ   | 884   | ö          | -             | 50 | 960:     | 20960       | Homo sapi |
|       | 10  | 88    | ő.         | 2             | 0  | 1254     | 3254        |           |
|       | 11  | 880.5 | φ.         | 7             | 14 | 6901     | 30691       |           |
|       | 12  | 876   | 6          | _             | 29 | 960:     | 20961       |           |
|       | 13  | 87    | ω.         | Ч             | 29 | 960:     | 20962       |           |
|       | 14  | 858.5 | 7.         | 6             | 10 | 629      | 56292       |           |
|       | 15  | 846   | 9          | 2             | 14 | 852      | 7852        |           |
|       | 16  | 843   | è.         | æ             | 13 | BU841314 | 113         |           |
|       | 17  | 838   | 5          | ដ             | 10 | 3116     | 3116        |           |
|       | 18  | 833.5 | 5          | S             | 11 | TII      | 1804        |           |
|       | 19  | 82    | 5.         | 61            | 12 | 1790     | 1790        |           |
|       | 20  | 816   | ۳,         | R             | 10 | 3200     | 3200        |           |
|       | 21  | 815   | ω.         | æ             | 13 | 3372     | 3372        |           |
|       | 22  | 799   | ς.         | Н             | 12 | 3296     | 5296        |           |
|       | 23  | 792   | Η.         | 9             | 12 | 7441     | 7441        |           |
|       | 24  | 777   | 。          | Н             | 12 | BI649317 | 1931        |           |
|       | 25  | 756   | 8          | ч             | 10 | 5046     | 5046        |           |
|       | 56  | 733   | ٠.         | 9             | 12 | 5214     | 5214        |           |
|       | 27  | 727   | 5.         | æ             | 10 | 1309     | 1309        |           |
|       | 28  | 106   | θ.         | 9             | 12 | 3580     | 3580        |           |
|       | 29  | 704   | ω.         | 4             | 12 | 5560     | 5560        |           |
|       | 30  | 693.5 | ď.         | 7             | 12 | 333      | 703353      |           |
|       | 31  | 687   | ď.         | 2             |    | 5867     | 2867        |           |
|       | 32  | 989   | ä          | 9             |    | 5511     | 56511       |           |
|       | 33  | 670   | ö          | 7             | 10 | BF320679 | 3206        |           |
|       | 34  | 999   | ö          | 4             |    | 1955     | 11955       |           |
|       | 35  | 99    | ö          | 3             |    | 2261     | 2261        |           |
|       | 36  | 658.5 | ė,         | σ             |    | 3768     | 8768        |           |
|       | 37  | 653   | φ.         | 9             |    | 1688     | 7688        |           |
|       | 38  | 651   | ω.         | α             |    | 5517     | 5517        |           |
|       | 39  | 651   | 8          | 2             |    | 1717     | 1717        |           |
|       | 40  | 650   | φ,         | ~             |    | 9699     | 9699        |           |
| ນ<br> | 41  | 649   | œ,         | æ             |    | 3645     | 3645        |           |
|       | 42  | 645   | ω.         | œ             |    | 1761     | 24761       |           |
|       | 43  | 639   | 7.         | $\vdash$      |    | 5978     | 26978       | BY269783  |
|       | 44  | 639   | ۲.         | 9             |    | 5071     | 6071        | BY26071   |
|       | 45  | 638   | 7.         | ø             |    | 1323     | 24323       | BY24323   |
|       |     |       |            |               |    |          |             |           |

ALIGNMENTS

BF160330 1091 bp mRNA linear EST 30-OCT-2000 601768601F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3987745 5', Mus musculus (house mouse)
Mus musculus
Mus musculus
Muscaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Musinae; Musinaes 1 to 1091) BF160330.1 GI:11040541 mRNA sequence. BF160330 EST. RESULT 1 BF160330 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

REFERENCE

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160 luSerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1004
197
5
                                                                                                                                         200 ProGluGlyProAlaAsnSerSerLysThrCysTrpCys 212
                                                                                                                                                                           676 cccrececcaccaaarcrrcaaagaacreccrecrec 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .1004
/organism="Mus musculus"
/mol_type="mRNA"
/strain="tVB/N-3"
/db xref="taxon:10090"
/clone="IMAGE:6515476"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-817-198C-2 (1-212) x BU517848 (1-1004)
                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                               BU517848
BU517848.1 GI:22825374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.85e-107
988.00
98.06%
95.63%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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/clone="IMAGE:3987745"
/tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab host="Origin."
/lab host="NCI_CGAP_Lu29"
/note="Organ: lung, Vector: pCWV-SPORT6; Site 1: Sall;
Site 2: NOtl; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:
http://inage.llnl.gov
Plate: LiAM9195 row: b column: 02
High quality sequence stop: 654.
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Conservative:
Mismatches:
Indels:
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/mol_type="mRNA"
/strain="Czech II"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. B. 1 (bases 1 to 1004)

E 1 (bases 1 to 1004)

NH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Biosciaence Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Llocation/Qualifiers

Llocation/Qualifiers
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/dev stage="5 months"
/dev stage="5 months"
/dev stage="5 months"
/dev stage="5 months"
/clone_lib="NHI CGAP Mam2"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site 1: Sall;
/note="Organ: mammary; Vector: pCNV-SPORT6; Site 1: Sall;
/ibrary constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NHH"
                                                                          180 euArgMetArgAlaSer-AsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyGlyFlys 199
                                                                                                                  153 ATGGCGAAACAGTACGATGTGCTGTTCCGGCTACTGCTGATCGGGGGACTCCGGGGTTGGC 212
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556 AGTCCTTCACTCGTCTGACGGAGCTGGTGCTGCAGGCCCCACAGGAAAGAGCTGGATGGTC
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/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: Ont; Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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BI648588.1 GI:15562824
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Matches:
Conservative:
Mismatches:
Indels:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (Bases I to 922)
NIH-MGC http://mgc.nci.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Geffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
R column: 09
High quality sequence stop; 685.
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602054039FI NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4193456 5',
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                                                                                                                                                     GCCCAGGGAATATTTTTAGTCTACGACATTAGCAGTGAGCGCTCCTATCAGCATGA
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140

564

624

684

504

444

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6035230888F1 CSEQCHN68 Gallus gallus cDNA clone ChEST465o22 5', mRNA
   Gallus gallus
Gallus Gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (Dases 1 to 759)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., A. Comgrehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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                                                                                                                                                                                                                                  LysThrCysTrpCys 212
                                                                                                                                                                                                                                                                                          564 AAGACCTGCTGGTGC 578
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Best Local Similarity:
Query Match:
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                                                                                     Contact: Robert Strausherg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at:
http://image.lln.gov
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High quality sequence stop: 614.
Location/Qualifiers
I. .616
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Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 GlufyralaProGluGlyValGlnLysileLeuileGlyAsnLysAlaAspGluGluGluGln 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 GAGTACGCTCCAGAAGGAGTCCAGAAGATCCTAATTGGGAATAAGGCTGATGAAGAGCAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 TyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGlu 167
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mismatches:
Indels:
Gaps:
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Site_2: Not1; Cloned unidirectionally.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
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High quality sequence stop: 706.
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Location/Qualifiers
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01753464F1 NCI_CGAP_Maml Mus musculus CDNA clone IMAGE:3981183 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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                                                                                                                                                                                                                                                      122 GACTTCAAGATGAAGACGATCGAGGTGGCATCAAGGTGCGCATCCAGATCTGGGAC 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 992)
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                                                                     GlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLysThrCys
                                                                                            24 LeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSIThrIleGlyVal
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   Gaps:
                                     US-09-817-198C-2 (1-212) x BU343508 (1-759)
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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BF101730
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433

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//note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BISS7933 699 bp mRNA linear EST 05-SEP-2001
                                                                                                                                                                         149 uThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGluLeuVa 169
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Mus musculus (house mouse)

Mus musculus

Mus musculus

Bukarda;

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 699)

11 (hases 1 to 699)

Nath-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CubNa Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11734 row: b column: 13
254 GCTCCAGAAGGAGTCCAGAAGATCCTAATTGGGAATAAGGCTGATGAAGAGCAGAAACGG
                                                                                                                                                                                                                                                                                                      189 aLeuAlaGluLeuGluGluGluGluGlyLysProGluGlyProAlaAsnSerSerLysTh
                                                                                                           374 AACAAGTGCCTGCACCAACCTTAAATATTTAAAGAGTCCTTCACTCGTCTGACGGAGGGTGGT
                                                                                                                                                                                                                                                                          169 lleuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArgAlaSerAsnGluLeuAl
                                                                          130 GlnValGlyArgGluGlnGlyGlnGlnLeuAlaLy8-GluTyrGlyMetAspPheTyrGl
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172
3
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .699
/organism="Mus musculus"
/mol type="mRNA"
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/db xref="taxon:10090"
/clone="IMAGE:5290284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 698.
Location/Qualifiers
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

I (bases 1 to 902)

SNIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

Contact: Robbert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

Contact: Preparation: Life Technologies, Inc.

Contact: DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

http://image.lln.gov

Plate: LiAM9320 row: £ column: 22

High quality sequence store: 2

High quality sequence store: 2

High quality sequence store: 3

Location/Qualifiers
                                                     BF178163 902 bp mRNA linear EST 31-OCT-2000
601809083F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4039701 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="texco":10090"
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/dev_stage="7 months"
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/lab host="0H108"
/clone lib="NUI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1;
/sle 2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 IleSerSerGluArgSerTyrGlnHigIleMetLygTrpValSerAspValAspGluTyr 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 ATCGAAGTAGACGGCATCAAAGTGATAATACAGATTTGGGACACAGCAGGGCAGGAGAGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
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Mismatches:
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    .902
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="C57BL/6J"

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                                                                                                           mRNA sequence.
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/mod_type="mRNA"
//mod_type="mRNA"
/db Arsf="taxon:10090"
/clone=llmHNGE:3078/643"
/lab host="lMAGE:3078/643"
/lab host="lMAGE:3078/643"
/lab host="lmH108 (change-resistant)"
/clone llb="NIH1 MGC 203"
/note="Organ: placenta; Vector: pExpress-1; Site 1: EcoRV;
Site 2: Not1; RNA obtained from three placentas from
Site 2: Not1; RNA obtained from three placentas from
Site 2: Not1; RNA obtained from three placentas from
Sine 1: Not1; RNA obtained from three placentas from
Sine 0: Not1; RNA extraction and purification (Tri-reagent method). cDNA was
primed using oligo-dT primer:
5'-pGACTGTTCTAGATCGCAGGCGCCCC(7)25-3' and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >lkb
resulted in an average insert size of 1.3 kb. This
primer; microquantity library is normalized to Cot5
(non-normalized primary library is normalized to Cot5
constructed by Express Genomics (Frederick, MD)."
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)

SM Mus musculus

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 773)

SM NIH-MOC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

LONDALished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: capapa-remail.nih.gov

Tissue Procurement: Naryam Bhat

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 706.

High quality sequence stop: 706.

Location/Qualifiers
                                                                                                                                                                                         CK030691 773 bp mRNA linear EST 26-NOV-2003 AGENCOURI 16648788 NIH MGC_203 Mus musculus cDNA clone IMAGE:30787643 5', mRNA sequence.
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563 TCTTTCACTCGTCTGACAGAGCTGGTCCTGATGGCTCAAAAGGGAGCTGGAGGGCTTG 622
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/organism="Mus musculus"
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                                                        181 Arg 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 ATAGGAGTTGACTTCAAAATGAAGACAATAGAGGTTGATGGGATCAAAGTAAGAATACAA 262
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                        Sanger Institute

Hinkton, Cambridgeshire, CB10 1SA, UK

Bamail: trop@sanger.ac.uk

Sanger Kenopus tropicalis BST project 2001

TROPICALIS_SEQUENCE ID: TEB9119f07.plkSP6

Sequencing primer: SP6

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

CDNA was oligo dT primed from Sug of poly A+ RNA from egg.

ECORI-NOIL cut cDNA was then ligated into pCS107 with ECORI at the

S' end and Noil at the 3' end.

Vector: pCS107; Site 1: ECORI; Site_2: NotI

Host: Escherichia coli XL1-blue.

Location/Qualifiers

rce
                                                                                                                                                                                                                                            egg.
EcoRI at t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AAGACCTGTTTGCTCTGCAGGTTCACAGACAACGAATTCCACCCTTCCCACACCATCCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="XGC-egg"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cE was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-Not cut cNNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetalaLysGlnTyrAspValLeuPheArgLeuLeuLeulleGlyAspSerGlyValGly
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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96.69%
92.27%
        Contact: Taylor R
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| /mol_type="genomic DNA"<br>/db_xref="taxon:9598" | gene <1>515<br>/locus_tag="HCM7398"<br>ORIGIN                      | Alignment Scores:  Pred. No.: Score: Score: 876.00 Matches: 169 Percent Similarity: 99.41% Conservative: 0 | : 99.41% Mismatches:<br>79.28% Indels:<br>29 Gaps:                  | US-09-817-198C-2 (1-212) x AY420961 (1-515) Qy 43 ValAspPheLySMetLysThrileGluValAspGlylleLysVal/ | . 63                                                             | . 8<br>8 . 63                                                            | DB 123 GGGATATITITIGGINNNCGACATITACCAGCGCGCTCTIACCAGG QY 103 VAISETASDVAIASDGIUTYTALAPTOGIUGIYVAIGINLYSTIE! | 123                                                                  | Db 243 GCIGAIGAGGAGCAGAAACGGCAGGIGGGAAGAGAGCAAGGGCAGG Qy 143 TyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsn: nh 303 TATGCARGAACTAGAACTAGACCACCAACCACCAACTAGAACTAGAAACTAGAAACTAGAAACTAGAAACTAGAACTAGAAACTAGAAACTAGAAACTAGAAACTAGAAACTAGAAACTAGAAACTAGAAACTAGAAACTAGAAACTAAAAAAAA | 163                                          | Qy 183 ArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGlu | Oy 203 ProAlaAsnSerSerLysThrCysTrpCys 212<br>                                                                                                                                        | RESULT 13 A7420962 LOCUS DEFINITION MUS musculus HCM7398 gene, VIRTUAL TRANSCRIPT, I | ACCESSION AY420962 GI:39776919 XEYWORDS GSS. | _                                                                                                                                                                                                                     | AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Todd, M.A., Tanabaum, D.M., Civello, D.R., Lu, F., | Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp             | JOURNAL Science 302 (5652), 1960-1963 (2003) PUBMED 14671302 |
|--------------------------------------------------|--------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|---------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|----------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|--------------------------------------------------------------|
| 142GGTGTTGACTTTAAGATG 159                        | 48 LysThrileGluValAspGlyIleLysValArgIleGlnileTrpAspThrAlaGlyGln 67 | GluargTyrGlnThrIleThrLysGlnTyrTyrargargalaGlnGlyIlePheLeuVal<br>                                           | 88 TyraspileSerSerGluargSerTyrGlnHisIleMetLysTrpValSeraspValAsp 107 | 108 GluTyrklaProGluGlyValGlnLysIleLeuIleGlyAsnLysklaAspGluGluGln 127<br>                         | LysargGlnValGlyargGluGlnGlyGlnGlnLeualaLysGluTyrGlyMetAspPhe<br> | 148 TyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGlu 167<br> | 168 LeuValLeuGinalaHisargiysGluLeuGluGlyGleuArgMetArgAlaSerAsnGlu 187<br>                                   | 188 LeualaLeualaGluLeuGluGluGluGluGlyLysProGluGlyProAlaAsnSerSer 207 | 208 LysThrCysTrpCys 212<br>                                                                                                                                                                                                                                                    |                                              | genomic survey sequence.<br>AY420961<br>AY420961.1 GI:39776918<br>GSS.          | Fan troglodytes (chimpanzee)<br>SM Pan troglodytes<br>Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,<br>Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan. | Cla<br>Tod<br>Fer                                                                    |                                              | <pre>2 (bases 1 to 515) 3 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,</pre> | _                                                                                                               | This sequence as made by sequencing genomic exons and ordering them based on alignment. | source 1515<br>/organism="Pan troglodytes"                   |
| qa                                               | ර සි                                                               | · 중 음                                                                                                      | <b>중</b> 음                                                          | <i>&amp;</i> €                                                                                   | \dot \d                                                          | & g                                                                      | දු දු                                                                                                       | & 원                                                                  | 6 G                                                                                                                                                                                                                                                                            | RESULT 12<br>AY420961<br>LOCUS<br>DEFINITION | ACCESSION<br>VERSION<br>KEYWORDS                                                | ORGANISM                                                                                                                                                                             | REFERENCE<br>AUTHORS<br>TITTE                                                        | JOURNAL<br>PUBMED                            | REFERENCE<br>AUTHORS                                                                                                                                                                                                  | TITLE<br>JOURNAL                                                                                                | COMMENT                                                                                 | 08                                                           |

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linear GSS 12-DEC-2003 [PT, partial sequence,
                         ysileLeuileGlyAsnLys 122
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                                                                                                                                                                                                                                                                                                             rtebrata; Euteleostomi;
; Muridae; Murinae; Mus.
ysvalargileginiletrp 62
                                                                                                                                                                                                                                                                                                                                                          chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                               as,P., Kejariwal,A.,
u,F., Murphy,B.,
J., Sninsky,J.J.,
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| SOURCE Home sapiens (human) ORGANISM Home sapiens (human) ORGANISM Home sapiens (bordata; Craniata; Vertebrata; Euteleostomi; Manmalia Euteria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE I (Dasse 1 to 796) AUTICE NUM-MUC http://mgc.nci.nih.gov/. INTLE NUM-MUC http://mgc.nci.nih.gov/. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Strauberg, Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert PH.D. COTHECT: Robert Ph.D. COTHECT: Robert Ph.D. COTHECT: Robert  | Alignment Scores: Pred. No.: Pred. No.: Score: Score: Score: Percent Similarity: 75.77\$ Conservative: 2 Best Local Similarity: 75.00\$ Ouery Match: 10 BB: 10 Gaps: 1                                                                                                                                                                                             | US-09-817-198C-2 (1-212) x BF966292 (1-796)   US-09-817-198C-2 (1-212) x BF966292 (1-796)   US-09-817-198C-2 (1-212) x BF966292 (1-796)   US-09-817-198C-3   US-09- |
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| AUTHORS Clark.A.G., Glanowaki.S., Nielson.R., Thomas, P.; Kejariwal.A., Todak, A., Tanenbaum, D.M., Civello, D.R., Lu.F., Murphy.B., Todak, M.A., Tanenbaum, D.M., Civello, D.R., Lu.F., Murphy.B., Todak, M.A., Mang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 20850, USA and Cargill, M. 208 | Qy         103 ValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLys         122           Db         183 GTCAGTGACGTGGATGACTACCCTCCAGAAGACTCCTGAAGATCCTAATTGGGAATAAG         242           Qy         123 AlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGlu         142           Db         243 GCTGATGAAGAGCAGAAAACGGCAGGAGAGAGAGAGCAGCAGCAGC | QY         143 TyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPhe 162           Db         303 TACGGCATGGACTTCTACGAAACAGCCTCCACCACCTTAATATTAAAGAGTCCTTC 362           QY         163 ThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMet 182           Db         363 ACTCGTCTGACGAGGCTGGTGCTGCAGGCCCACAGAAAGACTGCATGCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |

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//done="taxon:0116"
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//clone="type-ctor: pSPORT1; Site 1: Sal1; Site 2: Not1; W Rat hypothalamus adult female Wistar rat avg. insert size 2:3 kb fraction 6 and 7"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                      369 GGTGCCTCACCGGGGAAGGCAAGGCGAGGGCCAGATGGGAAGGCAAATGCTTCCAGGAAG
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                                 136 ATGGCGAAACAGTACGATGTGCTATTTCGGCTACTGCTGATCGGGGACTCCGGGGTGGGC
                                                                                                                                                                                                     IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                  LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerHisIleSerThr
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